

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 3, 2005, 16:07:30 ; Search time 71 Seconds
(without alignments)
1378.174 Million cell updates/sec

Title: US-10-509-691-2
Perfect score: 1363
Sequence: 1 MPTSDSGEPRIAMKNGVT.....SGEYFAPMDLSTTPGNSLK 253

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues
Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1363	100.0	253	3	AAg27962 Arabidops
2	1363	100.0	253	6	ABP81243 Arabidops
3	1363	100.0	253	7	ADL63897 Thale cre
4	1296	99.1	240	3	AAg27963 Arabidops
5	651	47.8	225	7	ADD30096 Plant yle
6	651	47.8	225	8	ADD31439 Plant yle
7	651	47.8	225	8	ADL44297 Plant tra
8	402	29.5	209	3	AAg36752 Arabidops
9	402	29.5	209	7	ADD30372 Arabidops
10	402	29.5	209	8	ADL44299 Plant tra
11	402	29.5	226	3	AAg36751 Arabidops
12	377.5	27.7	193	3	AAg41702 Arabidops
13	377.5	27.7	193	3	AAg41701 Arabidops
14	377.5	27.7	204	3	AAg41700 Arabidops
15	377.5	27.7	204	7	ADD30374 Arabidops
16	377.5	27.7	204	8	ADL41899 Plant tra
17	368.5	27.0	208	3	AAg39024 Arabidops
18	368	27.0	176	3	AAg12100 Arabidops
19	368	27.0	199	3	AAg12099 Arabidops
20	320.5	23.5	299	3	AAg23893 Arabidops
21	320.5	23.5	299	3	AAg23892 Arabidops
22	320.5	23.5	307	3	AAg47820 Arabidops
23	320.5	23.5	307	7	ADD30376 Plant yle
24	320.5	23.5	307	8	ADL44303 Plant tra
25	320.5	23.5	307	8	ADL44303 Plant tra

26	320	23.5	372	7	ADD30208
27	320	23.5	372	8	ADL43855
28	318	23.3	194	8	ADN74777 Thale cre
29	317.5	23.3	399	7	ADD30362 Plant yle
30	317.5	23.3	399	8	ADL44285 Plant tra
31	317	23.3	352	7	ADJ11580 Rice prot
32	316.5	23.2	271	3	AAg23894 Arabidops
33	316.5	23.2	271	3	AAg47822 Arabidops
34	316.5	23.2	275	6	AAE30054 Arabidops
35	316.5	23.2	275	7	ADD31015 Plant yle
36	316.5	23.2	275	8	ADL44307 Plant tra
37	312	22.9	339	3	AAg44195 Arabidops
38	312	22.9	353	3	AAg44194 Arabidops
39	309	22.7	338	3	AAg53237 Arabidops
40	309	22.7	338	7	ADB31873 Plant (a
41	309	22.7	338	7	ADC46609 Thalecres
42	309	22.7	338	8	ADD02089 Thalecres
43	309	22.7	352	3	AAg53236 Arabidops
44	308.5	22.6	271	3	AAg20543 Arabidops
45	308.5	22.6	271	3	AAg28857 Arabidops

ALIGNMENTS

RESULT 1	AAg27962 standard; protein, 253 AA.
ID	AAg27962
AC	AAg27962;
XX	
DT	17-OCT-2000 (first entry)
XX	
DE	Arabidopsis thaliana protein fragment SEQ ID NO: 33003.
XX	
KW	Protein identification; signal transduction pathway; metabolic pathway;
KW	hybridisation assay; genetic mapping; gene expression control; promoter;
KW	termination sequence.
OS	Arabidopsis thaliana.
PN	EP1033405-A2.
XX	
PD	06-SEP-2000.
XX	
PF	25-FEB-2000; 2000EP-00301439.
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PR	25-FEB-1999; 99US-0121825P.
PR	05-MAR-1999; 99US-0123180P.
PR	09-MAR-1999; 99US-0123548P.
PR	23-MAR-1999; 99US-0125788P.
PR	25-MAR-1999; 99US-0126264P.
PR	29-MAR-1999; 99US-0126785P.
PR	01-APR-1999; 99US-0127462P.
PR	06-APR-1999; 99US-0128234P.
PR	08-APR-1999; 99US-0128714P.
PR	16-APR-1999; 99US-0128845P.
PR	19-APR-1999; 99US-0130077P.
PR	21-APR-1999; 99US-0130449P.
PR	23-APR-1999; 99US-0130510P.
PR	23-APR-1999; 99US-0130891P.
PR	28-APR-1999; 99US-0131449P.
PR	30-APR-1999; 99US-0132048P.
PR	30-APR-1999; 99US-0132407P.
PR	04-MAY-1999; 99US-0132484P.
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PR	14-MAY-1999; 99US-0134221P.

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PR 23-JUL-1999;	99US-0145224P.	PR 25-OCT-1999;	99US-0160989P.
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PR 29-OCT-1999; 99US-0162142P.

Query Match 100.0%; Score 1363; DB 3; Length 253;
Best Local Similarity 100.0%; Pred. No. 2,2e-104;
Matches 253; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPTSDSGPRRIAMKPNVTVPISDQEQQLPCPRCDSSNTKFCYNNYNFSGPRHFCXAC 60
DB 1 MPTSDSGPRRIAMKPNVTVPISDQEQQLPCPRCDSSNTKFCYNNYNFSGPRHFCXAC 60
QY 61 RRYWTHGGTLRDVPVGGGTRKSAKSRCTSNSSSSSVSGVNSNGVPLQTTVPVLPPOSS 120
DB 61 RRYWTHGGTLRDVPVGGGTRKSAKSRCTSNSSSSSVSGVNSNGVPLQTTVPVLPPOSS 120
QY 121 ISNGVTHVTESDGGKSLSLCGSFTSTLNNHNAATATHGSGSVYIGIGFGIGSGGFD 180
DB 121 ISNGVTHVTESDGGKSLSLCGSFTSTLNNHNAATATHGSGSVYIGIGFGIGSGGFD 180
QY 181 DVSFGLGRAMPFSTVGTATTNNVSGNGHHAVPMPATWQFEGLESNAGGFGVSGEYPAW 240
DB 181 DVSFGLGRAMPFSTVGTATTNNVSGNGHHAVPMPATWQFEGLESNAGGFGVSGEYPAW 240
QY 241 PDLSTTTGNSLX 253
DB 241 PDLSTTTGNSLX 253

RESULT 2
ABP81243
ID ABP81243 standard; protein; 253 AA.

XX AC ABP81243;
XX DT 27-FEB-2003 (first entry)
XX DE Arabidopsis thaliana protein #71 modulated by PTGS.
XX KM Posttranscriptional gene silencing; PTGS; plant; transformation.
XX OS Arabidopsis thaliana.
XX PN WO200281695-A2.
XX PD 17-OCT-2002.
XX PF 05-APR-2002; 2002WO-EP003806.
XX PR 06-APR-2001; 2001US-0282049P.
XX PA (SYGN) SYNGENTA PARTICIPATIONS AG.
XX PA (FRIE-) FRIEDRICH MIESCHER INST.
XX PI Zhu T, Glazov EA, Meins F, Wang X, Chang H;
XX DR N-PSDB; AB242087.
XX PT Novel polynucleic acid segment useful for modulating gene expression
XX PT within a cell by posttranscriptional gene silencing, and for augmenting a
XX PT plant cell genome.
XX PS Claim 53; Page 301; 438pp; English.
CC The invention relates to a novel isolated polynucleic acid segment
CC modulated within a cell by posttranscriptional gene silencing (PTGS). The
CC invention specifically relates to a method to identify an expression

CC product that is modulated by PTGS. The polynucleotide is useful for
CC modulating the gene expression within a cell by PTGS, by introducing the
CC polynucleic acid into a cell and expressing the nucleic acid segment in
CC the cell to form a product. The polynucleic acid segment is also useful
CC for augmenting a cell genome, and for augmenting a plant genome, by
CC contacting a plant cell with the segment to produce a transformed plant
CC cell, and growing the transformed plant cell to produce a differentiated
CC transformed plant. The sequences shown in ABP81173 - ABP81298 represent
CC the product of a segment of A. thaliana cDNA modulated by PTGS

Query Match 100.0%; Score 1363; DB 6; Length 253;
Best Local Similarity 100.0%; Pred. No. 2,2e-104;
Matches 253; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPTSDSGPRRIAMKPNVTVPISDQEQQLPCPRCDSSNTKFCYNNYNFSGPRHFCXAC 60
DB 1 MPTSDSGPRRIAMKPNVTVPISDQEQQLPCPRCDSSNTKFCYNNYNFSGPRHFCXAC 60
QY 61 RRYWTHGGTLRDVPVGGGTRKSAKSRCTSNSSSSSVSGVNSNGVPLQTTVPVLPPOSS 120
DB 61 RRYWTHGGTLRDVPVGGGTRKSAKSRCTSNSSSSSVSGVNSNGVPLQTTVPVLPPOSS 120
QY 121 ISNGVTHVTESDGGKSLSLCGSFTSTLNNHNAATATHGSGSVYIGIGFGIGSGGFD 180
DB 121 ISNGVTHVTESDGGKSLSLCGSFTSTLNNHNAATATHGSGSVYIGIGFGIGSGGFD 180
QY 181 DVSFGLGRAMPFSTVGTATTNNVSGNGHHAVPMPATWQFEGLESNAGGFGVSGEYPAW 240
DB 181 DVSFGLGRAMPFSTVGTATTNNVSGNGHHAVPMPATWQFEGLESNAGGFGVSGEYPAW 240
QY 241 PDLSTTTGNSLX 253
DB 241 PDLSTTTGNSLX 253

RESULT 3
ADL63897
ID ADL63897 standard; protein; 253 AA.

XX AC ADL63897;
XX DT 20-MAY-2004 (first entry)
XX DE Thale cress drought tolerance 2 (DRO2) protein Segd 2.
XX KM Transgenic; plant; drought tolerance 2; DRO2; abiotic stress;
XX KM salt stress; freezing; protectant; agricultural crop; thale cress.
XX OS Arabidopsis thaliana.
XX PN WO2003081988-A2.
XX PD 09-OCT-2003.
XX PF 27-MAR-2003; 2003WO-US009479.
XX PR 27-MAR-2002; 2002US-0368650P.
XX PA (AGRI-) AGRINOMICS LLC.
XX PI Van Winkle J, Liu XL, Fitch JR, Shulaev V;
XX DR N-PSDB; ADL63896.
XX PT New transgenic plants comprising the drought tolerant 2 (DRO2) gene and
XX PT having increased tolerance to drought, useful in generating crops and/or
XX PT other plant species having improved ability to survive in low water
XX PS Claim 1; SEQ ID NO 2; 23pp; English.

XX This invention relates to generating novel transgenic plants with an
CC improved drought tolerance phenotype. Specifically, it relates to plants
CC transfected with a vector containing a heterologous drought tolerant 2
CC (DRO2) gene. The present invention describes the development of
CC genetically modified plants that overexpress the DRO2 gene, such that the
CC overall health of the transgenic plant is improved compared to controls
CC and in particular it displays increased tolerance to other abiotic
CC stresses including salt stress and freezing. Accordingly, such
CC compositions are plant protectants and hence are useful for the
CC generation of agricultural crops such as cotton, wheat, corn and beans
CC that exhibit an improved ability to survive in low water conditions. This
CC polypeptide sequence is the thale cress DRO2 protein sequence of the
CC invention.

XX Sequence 253 AA;

Query Match 100.0%; Score 1363; DB 7; Length 253;
Best Local Similarity 100.0%; Pred. No. 2,2e-104;
Matches 253; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPTSDSGPRRIAMKPNQVTPISDQEOQLPCPRCDSSNTKFCYNNYNEQPHFKAC 60
Db 1 MPTSDSGPRRIAMKPNQVTPISDQEOQLPCPRCDSSNTKFCYNNYNEQPHFKAC 60
QY 61 RRYWTHGGTLRDVVGCGTRKSAKRSRTCSNSSSSVSGVSNNGVPLQTTPLFPQSS 120
Db 61 RRYWTHGGTLRDVVGCGTRKSAKRSRTCSNSSSSVSGVSNNGVPLQTTPLFPQSS 120
QY 121 ISNGVTHVTESDQKGSALICGSFTSTLLNHNAAATHTHSGSVIGIGGFGIGLGSQFD 180
Db 121 ISNGVTHVTESDQKGSALICGSFTSTLLNHNAAATHTHSGSVIGIGGFGIGLGSQFD 180
QY 181 DVSFGLGRAMPFSTVGATTTNGSNGHVAVMPATWQEGLESNAGGFVSGEYFAW 240
Db 181 DVSFGLGRAMPFSTVGATTTNGSNGHVAVMPATWQEGLESNAGGFVSGEYFAW 240
QY 241 PDLSTTPGNSLK 253
Db 241 PDLSTTPGNSLK 253

RESULT 4
AAG27963
ID AAG27963 standard; protein; 240 AA.
XX
AC AAG27963;
XX
DT 17-OCT-2000 (first entry)
XX
DE Arabidopsis thaliana protein fragment SEQ ID NO: 33004.
XX
KM Protein identification; signal transduction pathway; metabolic pathway;
KM hybridisation assay; genetic mapping; gene expression control; promoter;
KM termination sequence.
XX
OS Arabidopsis thaliana.
XX
PN EPI033405-A2.
XX
PD 06-SEP-2000.
XX
PF 25-FEB-2000; 2000EP-00301439.
XX
PR 25-FEB-1999; 99US-0121825P.
PR 05-MAR-1999; 99US-0123180P.
PR 09-MAR-1999; 99US-0123548P.
PR 23-MAR-1999; 99US-0125788P.
PR 25-MAR-1999; 99US-0126264P.
PR 29-MAR-1999; 99US-0126785P.
PR 01-APR-1999; 99US-0127462P.
PR 06-APR-1999; 99US-0128234P.
PR 08-APR-1999; 99US-0128714P.

PR 16-APR-1999; 99US-0129845P.
PR 19-APR-1999; 99US-0130077P.
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PR 23-APR-1999; 99US-0130510P.
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PR 05-MAY-1999; 99US-0132485P.
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PR 06-MAY-1999; 99US-0132487P.
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PR 25-MAY-1999; 99US-0136021P.
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PR 03-JUN-1999; 99US-0137528P.
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PR 07-JUN-1999; 99US-0137724P.
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PR 14-JUL-1999; 99US-0143624P.
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PR 19-JUL-1999; 99US-0144333P.

	Query Match	95.1%: Score 1296; DB 3; Length 240;	
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PR	21-OCT-1999;	99US-0160767P.	
PR	21-OCT-1999;	99US-0160768P.	
PR	21-OCT-1999;	99US-0160770P.	
PR	21-OCT-1999;	99US-0160814P.	
PR	22-OCT-1999;	99US-0160815P.	
PR	22-OCT-1999;	99US-0160980P.	
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PR	22-OCT-1999;	99US-0160989P.	
PR	25-OCT-1999;	99US-0161404P.	
PR	25-OCT-1999;	99US-0161405P.	
PR	25-OCT-1999;	99US-0161406P.	
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PR	26-OCT-1999;	99US-0161360P.	
PR	26-OCT-1999;	99US-0161361P.	
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PR	28-OCT-1999;	99US-0161922P.	
PR	28-OCT-1999;	99US-0161932P.	
PR	29-OCT-1999;	99US-0162142P.	
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QY	74 PVGGGTTRSAKSRFTCSNSSSSSVGCVNSNGVPLQTTPLYFPOSTLSNGVTHVTESD	133	
Db	61 PVGGGTTRSAKSRFTCSNSSSSSVGCVNSNGVPLQTTPLYFPOSTLSNGVTHVTESD	120	
QY	134 GKGSALSLGSEFTSTLLNHNAAATATHTGSGSVYIGIGFGIGLGSGRDVSFGLGRAMWPF	193	
Db	121 GKGSALSLGSEFTSTLLNHNAAATATHTGSGSVYIGIGFGIGLGSGRDVSFGLGRAMWPF	180	
QY	194 STVGATTTTNGSNGCHAAVMPMATWQREGLSNNAGGVSEGEYFAMPDLSITTPGNSLK	253	
Db	181 STVGATTTTNGSNGCHAAVMPMATWQREGLSNNAGGVSEGEYFAMPDLSITTPGNSLK	240	
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ADD30096			
ID	ADD30096	standard; protein; 225 AA.	
XX	AC	ADD30096;	
XX	DT	15-JAN-2004 (first entry)	
XX	XX		
XX	XX	Plant yield-related protein from clone G1897.	
XX	XX	transcription factor; transgenic plant; growth rate; senescence;	
XX	XX	seed germination rate; plant vigor; seedling vigor.	
XX	OS	Arabidopsis thaliana.	
XX	PN	WO2003013227-A2.	
XX	XX		
XX	XX	20-FEB-2003.	
XX	XX		
XX	XX	09-AUG-2002; 2002WO-US025805.	
XX	XX		
XX	XX	09-AUG-2001; 2001US-0310847P.	
XX	XX	11-NOV-2001; 2001US-0336049P.	
XX	XX	11-DEC-2001; 2001US-0338692P.	
XX	XX	14-JUN-2002; 2002US-00171468.	
XX	XX		

PA	(MENDEL BIOTECHNOLOGY INC.
XX	
P1	Ratcliffe O, Riechmann JU, Adam LJ, Dubell AT, Heard JE,
P1	Pilgrimage M, Jiang C, Reuber TL, Creelman RA, Pineda O, Yu G;
P1	Brown PE;
XX	
DR	WPI; 2003-248221/24.
DR	N-PSDB; ADD30095.
XX	
PT	New plant transcription factor polynucleotides and polypeptides, useful
PT	in producing transgenic plants with commercially valuable properties,
PT	such as an alteration in a plant growth characteristic, e.g. growth rate
PT	or apomixis.
PS	Disclosure; SEQ ID NO 125; 454pp; English.
XX	
CC	The invention relates to a number of isolated Arabidopsis thaliana cDNA
CC	sequences and their encoded proteins which are especially transcription
CC	factor related cDNAs and proteins. The isolated or recombinant plant
CC	transcription factor polynucleotides and polypeptides are useful in
CC	producing transgenic plants with commercially valuable properties, i.e.
CC	modified or altered desirable traits as compared to a reference plant,
CC	such as an alteration in a plant growth characteristic, e.g. growth rate,
CC	germination rate of seeds, vigor of plants and seedlings, or leaf and
CC	flower senescence. Sequence information related to the polynucleotides
CC	and polypeptides can also be used in bioinformatic search methods. The
CC	transgenic plant is useful for growing a progeny plant from a parent
CC	plant. This sequence represents one of the proteins of the invention.
XX	
SQ	Sequence 225 AA;
	Query Match 47.8%; Score 651; DB 7; Length 225;
	Best Local Similarity 55.5%; Pred. No. 1.4e-45;
	Matches 137; Conservative 31; Mismatches 49; Indels 30; Gaps 10;
OY	1 MPTDSDGSPRRIAMKPN-----VWPRIIDQOEOLEPCPRCDSSNTRFCYNNYNVSQPENH 56
Db	1 MP-SFSSSRVPKIPHQGGGSVALP-TDOEQQLSCPCSESTNTKFCYNNYNVSQPHH 58
OY	57 CKACRRVYTHGTLDIVPGVGGRKSAKRSTRCSNSSSVSGVNSNGNPLOTTPULF 116
Db	59 CKSCRVRVYTHGTLDIPIVGVGRSSRSRSTRYSAAITTSVVG-----SRNPPLATPYLF 114
OY	117 PQSISINCVHTTVTESDGKSALSLCGSFSTLTLMNNAAPATTHGSGSVIGIGFGIGLG 176
Db	115 PQSSSNGGIT-----TAKGASNSFYGGF-SLLIYNNAAVRNBPQGCFNPDAFGILGLG 167
OY	177 SG--FDVVSFGIGRAMMPFTVTGT--ATTYVWSGCHHAHPMPTAQFEGLESNAGGCF 232
Db	168 HGYVEEDRVYOGGITVWFPPSSGADDAITTS-----HIQIRATWQFEQDSKV--GF 218
OY	233 VSGEYFA 239
Db	219 VSGDYVA 225
RESULT 6	
ADEJ1439	
ID	ADEJ1439 standard; protein; 225 AA.
AC	
XX	ADEJ1439;
DT	29-JAN-2004 (first entry)
XX	
DE	Plant yield related protein from clone G1897.
XX	
KM	transcription factor; transgenic plant; salt stress resistance;
KM	osmotic stress resistance; freezing tolerance; drought tolerance;
XX	low humidity tolerance; radiation resistance.
OS	Arabidopsis thaliana.
SN	WO2003013228-A2.

[illegible]

DE Plant transcription factor related polypeptide #1737.
 XX transgenic; plant; enhanced tolerance to abiotic stress;
 KW glyophosphate tolerance; hormone sensitivity; disease resistance;
 KW sugar sensing; flowering; flower structure; stem bifurcation;
 KW branching pattern; apical dominance; trichome; stem morphology;
 KW root growth; root hair; seed development; cell proliferation;
 KW cell differentiation; premature senescence; necrosis; plant size;
 KW leaf morphology; seed morphology; seed biochemistry; root anthocyanin;
 KW plant anthocyanin; light response; shade avoidance; bioinformatic;
 KW transcription factor; db.
 XX Unidentified.
 OS
 XX US2004019927-A1.
 PN
 XX 29-JAN-2004.
 PD
 XX 25-FEB-2003; 2003US-00374780.
 PF
 XX 18-APR-2001; 2001US-00837944.
 PR
 XX (SHER/) SHERMAN B K.
 PA (RIEC/) RIECHMANN J L.
 PA (JIAN/) JIANG C.
 PA (HEAR/) HEARD J E.
 PA (HAAK/) HAAKE V.
 PA (CREE/) CREELMAN R A.
 PA (RATC/) RATCLIFFE O.
 PA (ADAM/) ADAM L J.
 PA (REUB/) REUBER T L.
 PA (KEDD/) KEDDIE J.
 PA (BROU/) BROUN P E.
 PA (PILG/) PILGRIM M L.
 PA (DUBE/) DUBBEL A N.
 PA (PINE/) PINEDA O.
 PA (YUGG/) YU G.
 XX
 PI Sherman BK, Riechmann JL, Jiang C, Heard JE, Haake V;
 PI Creelman RA, Ratcliffe O, Adam LJ, Reuber TL, Keddie J, Broun PE;
 PI Pilgrim ML, Dubell AN, Pineda O, Yu G;
 DR WP1; 2004-132245/13.
 DR N-PSDB; ADI44296.
 XX
 PT New transgenic plant comprising a recombinant polynucleotide of any one
 PT of more than 500 nucleotide sequences, useful in bioinformatic search
 PT methods.
 PS
 XX Disclosure; SEQ ID NO 2760; 435bp; English.
 CC The invention describes a transgenic plant comprising a recombinant
 CC polynucleotide of any one of more than 500 nucleotide sequences fully
 CC defined in the specification or its complement. The method of the
 CC invention can be used to produce a plant having altered traits such as:
 CC enhanced tolerance to abiotic stress; glyophosphate tolerance; hormone
 CC sensitivity; disease resistance; sugar sensing; early or late flowering;
 CC altered flower structure; change in stem bifurcations; altered branching
 CC pattern; reduced apical dominance; reduced trichome density; lack of
 CC trichomes; reduced ectopic trichome development; altered trichome
 CC development; increase in trichome number; altered stem morphology;
 CC increased root growth; increased root hairs; altered seed development;
 CC altered cell proliferation or cell differentiation; rapid development;
 CC premature senescence; increased necrosis; increase in seedling or plant
 CC size; decreased plant size; leaf morphology; seed morphology; plant
 CC biochemistry; increase in root anthocyanins; increase in plant
 CC anthocyanins; or alteration in light response or shade avoidance. The
 CC transgenic plant, polynucleotides and polypeptides are useful in
 CC bioinformatic search methods. This sequence represents a plant
 CC transcription factor related polynucleotide.
 XX
 SO Sequence 225 AA;

Query Match 47.8%; Score 651; DB 8; Length 225;
 Best Local Similarity 55.5%; Pred. No. 1,4e-45;
 Matches 137; Conservative 31; Mismatches 49; Indels 30; Gaps 10;
 QY 1 MPTSDSGEPRRIAMKPNG---VTVPIDQEQLPQPCDSSNTYFCYYNNNTFSQPRHF 56
 DB 1 MP-SFSSRSRRPDKIPHCQGSVAIP-IDQEQQLSCPCESTNTFCYYNNNTFSQPRHF 58
 QY 57 CKACRRYTHGCTADVDVGGGTRSAKRSRSCSSSSSVSGVNSNGVLOTTPVLF 116
 DB 59 CKSCRRYTHGCTADVDVGGGTRSAKRSRSCSSSSSVSGVNSNGVLOTTPVLF 114
 QY 117 POSSISNGVTHTVTESDGKSALSLGSEFTSTLNNNAATATHGSGSVTIGCGIGLG 176
 DB 115 POSSSNGGIT-----TAKGSASSFYCGF-SGLIYNNAVSNRGCGGNGPDAFGLGIG 167
 QY 177 SG-FDDVSPGLGRAMPFSTVGT--ATTNVGNGGHHAVMPATWQFEGLESNAGGF 232
 DB 168 HGSYYEDVRYGQGITVWPFSSGATDAATTTT-----HIAQIPATWQFEGQSHV--GF 218
 QY 233 VSGEYFA 239
 DB 219 VSGDYVA 225
 RESULT 8
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 ID AAG36752 standard; protein; 209 AA.
 XX AAG36752;
 AC
 XX 18-OCT-2000 (first entry)
 DT
 XX Arabidopsis thaliana protein fragment SEQ ID NO: 45085.
 DE
 XX Protein identification; signal transduction pathway; metabolic pathway;
 KW hybridisation assay; genetic mapping; gene expression control; promoter;
 KW termination sequence.
 XX Arabidopsis thaliana.
 OS
 XX Arabidopsis thaliana.
 PN
 XX EP1033405-A2.
 PD
 XX 06-SEP-2000.
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 PF 25-FEB-2000; 2000EP-00301439.
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PR 29-SEP-1999; 99US-0156567P.
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PR 14-OCT-1999; 99US-0159637P.
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PR 18-OCT-1999; 99US-0159584P.
PR 18-OCT-1999; 99US-0160741P.
PR 21-OCT-1999; 99US-0160767P.
PR 21-OCT-1999; 99US-0160768P.
PR 21-OCT-1999; 99US-0160770P.
PR 21-OCT-1999; 99US-0160814P.
PR 21-OCT-1999; 99US-0160815P.
PR 22-OCT-1999; 99US-0160980P.
PR 22-OCT-1999; 99US-0160981P.
PR 22-OCT-1999; 99US-0160989P.
PR 25-OCT-1999; 99US-0161404P.
PR 25-OCT-1999; 99US-0161405P.


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PR 25-OCT-1999; 99US-0161406P.
PR 26-OCT-1999; 99US-0161359P.
PR 26-OCT-1999; 99US-0161360P.
PR 26-OCT-1999; 99US-0161361P.
PR 28-OCT-1999; 99US-0161920P.
PR 28-OCT-1999; 99US-0161922P.
PR 28-OCT-1999; 99US-0161932P.
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PR 29-OCT-1999; 99US-0162142P.

Query Match 29.5%; Score 402; DB 3; Length 209;
Best Local Similarity 39.0%; Pred. No. 4.8e-25;
Matches 101; Conservative 35; Mismatches 67; Indels 56; Gaps 13;

QY 1 MPTSDSGPRRIAMKPNKNGVTVPISDQOQLPCPRCDSNTKFCYNNYNNFSQPRHFCAC 60
DB 1 MP-SEPNQTRPTRVQPSFAAYPPVLAEPPLPCPRCNSSTTKFCYNNYNNLAQPRYCKSC 59

QY 61 RRYWTHGGTLADVPVGGGTRK-SAKRSRTCSN--SSSSVSGVYNSNGVPLQTPVLP 117
DB 60 RRYWTHGGTLADVPVGGGTRSSSRHRSFSTTATSSSSSVITTTQEPATTEA---S 116

QY 118 QSSISNGVHTVTESDQKGSALSLCGSFTSTLLNHNAAATATHSGSVIGIG--FGIGL 175
DB 117 QTKYTNLIS-----GHGSPASLLGL-----GSGN---GGLDYGRGY 149

QY 176 GSGFDVVSFG-LGRAMPFSTVGTATTNNVSGNGHNAVPMATWQFGLSNGGGRVS 234
DB 150 GYGLEMSIGYIGD-----SSVGEIPV--VDGCGD-----TWQIGELIGKSG----- 190

QY 235 GEYFAMPDLSTTPGNSLX 253
DB 191 GDSLWPGLEISMOTNDVK 209

RESULT 9
ADD30372
ID ADD30372 standard; protein; 209 AA.
XX
AC ADD30372;
XX
DT 15-JAN-2004 (first entry)
XX
DE Plant yield-related protein from clone G1898.
XX
KW transcription factor; transgenic plant; growth rate; senescence;
XX seed germination rate; plant vigor; seedling vigor.
XX
OS Arabidopsis thaliana.
XX
PN WO2003013227-A2.
XX
PD 20-FEB-2003.
XX
PF 09-AUG-2002; 2002WO-US025805.
XX
PR 09-AUG-2001; 2001US-0310847P.
PR 19-NOV-2001; 2001US-0336049P.
PR 11-DEC-2001; 2001US-0338692P.
PR 14-JUN-2002; 2002US-00171468.
XX
PA (MEND-) MENDEL BIOTECHNOLOGY INC.
XX
PI Ratcliffe O, Riechmann JL, Adam LJ, Dubell AT, Heard JB;
PI Pilgrim WL, Jiang C, Reuber TL, Creelman RA, Pineda O, Yu G;
PI Broun PE;
XX
XX MPI; 2003-248221/24.
XX
XX N-PSDB; ADD30371.
XX
XX New plant transcription factor polynucleotides and polypeptides, useful
XX in producing transgenic plants with commercially valuable properties,
XX PT such as an alteration in a plant growth characteristic, e.g. growth rate
XX or apomixis.
```

```
XX
PS Disclosure; SEQ ID NO 401; 454bp; English.
XX
CC The invention relates to a number of isolated Arabidopsis thaliana cDNA
CC sequences and their encoded proteins which are especially transcription
CC factor related cDNAs and proteins. The isolated or recombinant plant
CC transcription factor polynucleotides and polypeptides are useful in
CC producing transgenic plants with commercially valuable properties, i.e.
CC modified or altered desirable traits as compared to a reference plant,
CC such as an alteration in a plant growth characteristic, e.g. growth rate,
CC germination rate of seeds, vigor of plants and seedlings, or leaf and
CC flower senescence. Sequence information related to the polynucleotides
CC and polypeptides can also be used in bioinformatic search methods. The
CC transgenic plant is useful for growing a progeny plant from a parent
CC plant. This sequence represents one of the proteins of the invention.
XX
SQ Sequence 209 AA;

Query Match 29.5%; Score 402; DB 7; Length 209;
Best Local Similarity 39.0%; Pred. No. 4.8e-25;
Matches 101; Conservative 35; Mismatches 67; Indels 56; Gaps 13;

QY 1 MPTSDSGPRRIAMKPNKNGVTVPISDQOQLPCPRCDSNTKFCYNNYNNFSQPRHFCAC 60
DB 1 MP-SEPNQTRPTRVQPSFAAYPPVLAEPPLPCPRCNSSTTKFCYNNYNNLAQPRYCKSC 59

QY 61 RRYWTHGGTLADVPVGGGTRK-SAKRSRTCSN--SSSSVSGVYNSNGVPLQTPVLP 117
DB 60 RRYWTHGGTLADVPVGGGTRSSSRHRSFSTTATSSSSSVITTTQEPATTEA---S 116

QY 118 QSSISNGVHTVTESDQKGSALSLCGSFTSTLLNHNAAATATHSGSVIGIG--FGIGL 175
DB 117 QTKYTNLIS-----GHGSPASLLGL-----GSGN---GGLDYGRGY 149

QY 176 GSGFDVVSFG-LGRAMPFSTVGTATTNNVSGNGHNAVPMATWQFGLSNGGGRVS 234
DB 150 GYGLEMSIGYIGD-----SSVGEIPV--VDGCGD-----TWQIGELIGKSG----- 190

QY 235 GEYFAMPDLSTTPGNSLX 253
DB 191 GDSLWPGLEISMOTNDVK 209

RESULT 10
ADI44299
ID ADI44299 standard; protein; 209 AA.
XX
AC ADI44299;
XX
DT 22-APR-2004 (first entry)
XX
DE Plant transcription factor related polypeptide #1738.
XX
KW transgenic; plant; enhanced tolerance to abiotic stress;
KW glyophosphate tolerance; hormone sensitivity; disease resistance;
KW sugar sensing; flowering; flower structure; stem bifurcation;
KW branching pattern; apical dominance; trichome; stem morphology;
KW root growth; root hair; seed development; cell proliferation;
KW cell differentiation; premature senescence; necrosis; plant size;
KW leaf morphology; seed morphology; seed biochemistry; root anthocyanin;
KW plant anthocyanin; light response; shade avoidance; bioinformatic;
KW transcription factor; db.
XX
OS Unidentified.
XX
PN US2004019927-A1.
XX
XX 29-JAN-2004.
XX
XX 25-FEB-2003; 2003US-00374780.
XX
XX 18-APR-2001; 2001US-00837944.
XX
```

PA (SHER/) SHERMAN B K.
PA (RIEC/) RIECHMANN J L.
PA (JIANG/) JIANG C.
PA (HEAR/) HEARD J E.
PA (HAK/) HAKE V.
PA (CREE/) CREELMAN R A.
PA (RATC/) RATCLIFFE O.
PA (ADAM/) ADAM L J.
PA (REUB/) REUBER T L.
PA (KEDD/) KEDDIE J.
PA (BROU/) BROUN P E.
PA (PRIG/) PRIGIM M L.
PA (DUBE/) DUBELL A N.
PA (PINE/) PINEDA O.
PA (YUGG/) YU G.
PI Sherman BK, Riechmann JL, Jiang C, Heard JE, Hake V,
PI Creelman RA, Ratcliffe O, Adam LJ, Reuber TL, Keddie J, Broun PE,
PI Prigim ML, Dubell AN, Pineda O, Yu G;
XX WPI: 2004-132245/13.
DR N-PSDB; ADI44298.
XX
PT New transgenic plant comprising a recombinant polynucleotide of any one
PT of more than 500 nucleotide sequences, useful in bioinformatic search
PT methods.
PS Disclosure; SEQ ID NO 2762; 435pp; English.
XX
XX The invention describes a transgenic plant comprising a recombinant
XX polynucleotide of any one of more than 500 nucleotide sequences fully
XX defined in the specification or its complement. The method of the
XX invention can be used to produce a plant having altered traits such as:
XX enhanced tolerance to abiotic stresses; glyphosphate tolerance; hormone
XX sensitivity; disease resistance; sugar sensing; early or late flowering;
XX altered flower structure; change in stem bifurcations; altered branching
XX pattern; reduced apical dominance; reduced trichome density; lack of
XX trichomes; reduced ectopic trichome development; altered trichome
XX development; increased trichome number; altered stem morphology;
XX increased root growth; increased root hairs; altered seed development;
XX altered cell proliferation or cell differentiation; rapid development;
XX premature senescence; increased necrosis; increase in seedling or plant
XX size; decreased plant size; leaf morphology; seed morphology; seed
XX biochemistry; increase in root anthocyanins; increase in plant
XX anthocyanins; or alteration in light response or shade avoidance. The
XX transgenic plant, polynucleotides and polypeptides are useful in
XX bioinformatic search methods. This sequence represents a plant
XX transcription factor related polynucleotide.
SQ Sequence 209 AA;
Query Match 29.5%; Score 402; DB 8; Length 209;
Best Local Similarity 39.0%; Pred. No. 4.8e-25;
Matches 101; Conservative 35; Mismatches 67; Indels 56; Gaps 13;
QY 1 MPTSDSEPRRIAMKPGVTVPISDQQLPCPCDSSNTKFCYNNYNFSQPRHFCAC 60
DB 1 MP-SEPQRTPTRVQSTAAVPPNLAEPLEPCPCRNSTTTFYCYNNYNLAQPRXYCKSC 59
QY 61 RRYWTHGGTLRDVVGGGTRK-SAKRSRTCSN--SSSSSVGVSNGVNPLOTTPVLPF 117
DB 60 RRTWOGGTLRDVVGGGTRSSSKRRHSFSTNATSSSSSVTTTTOBEATTEA--S 116
QY 118 QSSISNGVTHVTESDCKGSLSCGSFTSTLHNNAATATHGSGSVIGIG--FGIGL 175
DB 117 QTKVTNLIIS-----GHGSPASLGL-----GSGN-----GGLDYGFY 149
QY 176 GSGFDVDFG-LGRAMPFSTVGTATTNNVSGNCHAAVMPATWQEGLESNAGGFFVS 234
DB 150 GYGLEMSIGTLD-----SSVGEIPV--VDGCGGD-----TWQIGETEGKSG----- 190
QY 235 GEYAWPDLSTTTGNSLK 253

DB 191 GDSLIMPGLISMQTNVCK 209
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ID AAG36751 standard; protein; 226 AA.
XX AAG36751;
AC
XX 18-OCT-2000 (first entry)
DT
XX Arabidopsis thaliana protein fragment SEQ ID NO: 45084.
XX Protein identification; signal transduction pathway; metabolic pathway;
XX hybridisation assay; genetic mapping; gene expression control; promoter;
XX termination sequence.
XX Arabidopsis thaliana.
XX EPI033405-A2.
XX
XX 06-SEP-2000.
XX
XX 25-FEB-2000; 2000EP-00301439.
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XX 25-FEB-1999; 99US-0121825P.
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Qy 235 GEYPAMPDLSTTPGNSLX 253
Db 208 GDSLWPFLEISMQNDVK 226
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ID AAG41702 standard; protein; 193 AA.
XX
AC AAG41702;
XX
DT 18-OCT-2000 (first entry)
XX
DE Arabidopsis thaliana protein fragment SEQ ID NO: 51918.
XX
KW Protein identification; signal transduction pathway; metabolic pathway;
KM hybridisation assay; genetic mapping; gene expression control; promoter;
XX termination sequence.
OS Arabidopsis thaliana.
XX
PN EPI033405-A2.
XX
PD 06-SEP-2000.
XX
PE 25-FEB-2000; 2000EP-00301439.
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PR	26-OCT-1999;	99US-0161360P.
PR	26-OCT-1999;	99US-0161361P.
PR	28-OCT-1999;	99US-0161920P.
PR	28-OCT-1999;	99US-0161922P.
PR	28-OCT-1999;	99US-0161935P.
PR	29-OCT-1999;	99US-0162142P.

Oy		26 QDSQLCPDPCDSDNTEFCYNNVYNPSODRHFCKARRWTHGGTLRDVPVGGRKSAKR	85
Dd		14 EDSQLCPDRDSDPNTKFTCYNNYNLSQPHFKSCRRRTWKGALRNVPVGGGSRKNATK	73
Oy		86 SFRCSNSSSSSVGVVSNNGVPLQTTPVLFPSSISNGVTHT-----VTESDGKGA	138
Dd		74 RSTSSSSSASSPEN--SQNKTKTKMPDDPDPPRNSQRPDLPTMLVGFPIGDVDYG--	129
Oy		139 LSLCGSFSTLLMHNMAAATATGSGSVIGIGFICGL-GSGFDVDSFRLG	187
Dd		130 MEIGGSFFSSILANN-----MOLGLGGGIMLDSGMHDHPMGMLG	168
RESULT 13			
ID	AAG41701		
ID	AAG41701 standard; protein; 194 AA.		
AC	AAG41701;		
XX			
DT	18-OCT-2000 (first entry)		
XX			
DE	Arabidopsis thaliana protein fragment SEQ ID NO: 51917.		
XX			
KM	Protein identification: signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.		
XX			
OS	Arabidopsis thaliana.		
PN	EPI033405-A2.		
XX			
PD	06-SEP-2000.		
XX			
PF	25-FEB-2000; 200DEP-00301439.		
XX			
PR	25-FEB-1999; 99US-0121825P.		
PR	05-MAR-1999; 99US-0123180P.		
PR	09-MAR-1999; 99US-0123548P.		
PR	23-MAR-1999; 99US-0125788P.		
PR	25-MAR-1999; 99US-0126264P.		
PR	29-MAR-1999; 99US-0126785P.		
PR	01-APR-1999; 99US-0127462P.		
PR	06-APR-1999; 99US-0128234P.		
PR	08-APR-1999; 99US-0128714P.		
PR	16-APR-1999; 99US-0129845P.		
PR	19-APR-1999; 99US-0130077P.		
PR	21-APR-1999; 99US-0130450P.		
PR	23-APR-1999; 99US-0130510P.		
PR	23-APR-1999; 99US-0130891P.		
PR	28-APR-1999; 99US-0131449P.		
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PR	14-MAY-1999; 99US-0134218P.		
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PR	14-MAY-1999; 99US-0134370P.		
PR	18-MAY-1999; 99US-0134768P.		
PR	19-MAY-1999; 99US-0134941P.		
PR	20-MAY-1999; 99US-0135124P.		
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PR	04-JUN-1999; 99US-0137502P.		

PR	06-JUN-1999	99US-01387224P
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PR	10-JUN-1999	99US-01388440P
PR	10-JUN-1999	99US-01388477P
PR	14-JUN-1999	99US-0139119P
PR	16-JUN-1999	99US-01394542P
PR	16-JUN-1999	99US-01394553P
PR	17-JUN-1999	99US-01394922P
PR	18-JUN-1999	99US-01394954P
PR	18-JUN-1999	99US-01394557P
PR	18-JUN-1999	99US-01394576P
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PR	02-JUL-1999	99US-0142055P
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PR	09-AUG-1999;	99US-01476932;
PR	09-AUG-1999;	99US-01479359;
PR	10-AUG-1999;	99US-0148171P;
PR	11-AUG-1999;	99US-01483199;
PR	12-AUG-1999;	99US-0148341P;
PR	13-AUG-1999;	99US-01485655;
PR	13-AUG-1999;	99US-01486849;
PR	16-AUG-1999;	99US-01493568P;
PR	17-AUG-1999;	99US-01491755P;
PR	18-AUG-1999;	99US-01495426P;
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PR	20-AUG-1999;	99US-01497923P;
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PR	23-AUG-1999;	99US-01499802P;
PR	23-AUG-1999;	99US-01499930P;
PR	25-AUG-1999;	99US-01505566P;
PR	26-AUG-1999;	99US-01508849P;
PR	27-AUG-1999;	99US-0151065P;
PR	27-AUG-1999;	99US-0151066P;
PR	30-AUG-1999;	99US-0151103P;
PR	31-AUG-1999;	99US-01515138P;
PR	01-SEP-1999;	99US-01515303P;
PR	07-SEP-1999;	99US-0152363P;
PR	10-SEP-1999;	99US-0153076P;
PR	13-SEP-1999;	99US-01537558P;
PR	15-SEP-1999;	99US-0154018P;
PR	16-SEP-1999;	99US-0154039P;
PR	20-SEP-1999;	99US-0154779P;
PR	22-SEP-1999;	99US-0155133P;
PR	23-SEP-1999;	99US-0155486P;
PR	24-SEP-1999;	99US-0155559P;
PR	28-SEP-1999;	99US-0156458P;
PR	29-SEP-1999;	99US-0156596P;
PR	04-OCT-1999;	99US-0157117P;
PR	05-OCT-1999;	99US-01575733P;
PR	06-OCT-1999;	99US-0157865P;
PR	07-OCT-1999;	99US-0158032P;
PR	08-OCT-1999;	99US-0158232P;
PR	12-OCT-1999;	99US-0158369P;
PR	13-OCT-1999;	99US-01592943P;
PR	13-OCT-1999;	99US-01592949P;
PR	14-OCT-1999;	99US-01595925P;
PR	14-OCT-1999;	99US-01595929P;
PR	14-OCT-1999;	99US-01593331P;
PR	14-OCT-1999;	99US-0159637P;
PR	18-OCT-1999;	99US-01595638P;
PR	18-OCT-1999;	99US-01595848P;
PR	21-OCT-1999;	99US-0160741P;
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PR	21-OCT-1999;	99US-0160768P;
PR	21-OCT-1999;	99US-0160774P;
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PR	21-OCT-1999;	99US-0160815P;
PR	22-OCT-1999;	99US-01609881P;
PR	22-OCT-1999;	99US-01609881P;
PR	25-OCT-1999;	99US-0161404P;
PR	25-OCT-1999;	99US-0161405P;
PR	26-OCT-1999;	99US-0161406P;
PR	26-OCT-1999;	99US-0161359P;
PR	26-OCT-1999;	99US-0161360P;
PR	26-OCT-1999;	99US-0161361P;
PR	28-OCT-1999;	99US-0161920P;
PR	28-OCT-1999;	99US-0161929P;
PR	29-OCT-1999;	99US-01621933P;
PR	29-OCT-1999;	99US-01621422P;

Query Match	27.7%;	Score 377.5;	DB 3;	Length 194;
Local Similarity	48.8%;	Pred. No. 4.6e-23;		
Matches 83;	Conservative 21;	Mismatches 43;	Indels 23;	Gaps 5;

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 3, 2005, 16:09:31 ; Search time 15 Seconds
(without alignments)
1622.856 Million cell updates/sec

Title: US-10-509-691-2
Perfect score: 1363
Sequence: 1 MPTSDSGPRIRAMKPNVGT.....SGEYFAMPDLSTTPGNSLK 253

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1033	75.8	195	2	T46072 DNA binding protei
2	402	29.5	209	2	E96517 hypothetical prote
3	377.5	27.7	204	2	T52045 DoF zinc finger pr
4	327	24.0	328	2	T02046 prolamn box bindi
5	320.5	23.5	225	2	S59852 DNA-binding protei
6	318	23.3	194	2	T52044 dof zinc finger pr
7	317.5	23.3	399	2	T48267 hypothetical prote
8	316.5	23.2	339	2	H86210 hypothetical prote
9	314.5	23.1	262	2	T02203 finger protein DoF
10	312.5	22.9	311	2	D86409 hypothetical prote
11	309	22.6	385	2	E96669 protein PIN1.19 l
12	308.5	22.6	234	2	T02370 finger protein BBF
13	308	22.6	356	2	G84904 probable DOF zinc
14	306.5	22.5	320	2	B84689 probable DOF zinc
15	305	22.4	245	2	T47501 doF6 zinc finger p
16	304	22.3	259	2	G84685 probable DOF zinc
17	294.5	21.6	296	2	T47977 transcription fact
18	294.5	21.6	361	2	T13450 hypothetical prote
19	293.5	21.5	238	2	S66358 DNA-binding protei
20	293.5	21.5	302	2	S59853 DNA-binding protei
21	290.5	21.3	278	2	F85012 hypothetical prote
22	290.5	21.3	575	2	T01552 hypothetical prote
23	290.5	21.3	238	2	T02373 finger protein BBF
24	286	21.0	330	2	T02525 probable DOF zinc
25	285	20.9	245	2	T05627 hypothetical prote
26	283.5	20.8	307	2	T47676 zinc finger protei
27	283	20.8	264	2	T50640 zinc finger protei
28	281.5	20.7	448	2	T45710 H-protein promoter
29	278.5	20.4	114	2	T02374 finger protein BBF

30	273	20.0	210	2	T10647 hypothetical prote
31	273	20.0	380	2	T09661 ascorbate oxidase
32	271	19.9	247	2	T08455 hypothetical prote
33	267.5	19.6	399	2	D96717 hypothetical prote
34	267.5	19.6	400	2	T51953 H-protein promoter
35	267	19.6	119	2	T02375 finger protein BBF
36	260.5	19.1	249	2	T04939 hypothetical prote
37	252.5	18.5	232	2	T10646 hypothetical prote
38	250.5	18.4	170	2	H84752 probable DOF zinc
39	178.5	13.1	194	2	T10645 hypothetical prote
40	123	9.0	1076	1	A35622 nuclear pore prote
41	122	9.0	963	2	T40290 hypothetical prote
42	113	8.3	749	2	I38488 trophinin - human
43	112.5	8.3	731	2	C70974 hypothetical glyci
44	112	8.2	1428	2	T08852 luciferin A - Califo
45	111.5	8.2	708	2	A53185 G-box-binding fact

ALIGNMENTS

RESULT 1

T46072 DNA binding protein - Arabidopsis thaliana (fragment)
N:Alernate names: protein T20E23.10
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 09-Jul-2004
C:Accession: T46072
R:Barques, M.; Perez-Derez, A.; Terol, J.; Torres, A.; Perez-Alonso, M.; Mewes, H.W.; Le
submitted to the Protein Sequence Database, December 1999
A:Reference number: 223020
A:Accession: T46072
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-195 <BAR>
A:Cross-references: UNIPROT:Q9M2R8; EMBL:AL133363
A:Experimental source: cultivar Columbia; BAC clone T20E23
C:Genetics:
A:Map position: 3
A:Note: T20E23.10

Query Match 75.8%; Score 1033; DB 2; Length 195;
Best Local Similarity 100.0%; Pred. No. 4.7e-68;
Matches 195; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	59	ACRRYTHGGLRDVPGGTRKSAKRRTSSSSSVSGVSNKVPLOTPVLPQ	118
DB	1	ACRRYTHGGLRDVPGGTRKSAKRRTSSSSSVSGVSNKVPLOTPVLPQ	60
QY	119	SSISNGVHTVTESDGKSAISLCSFTSTLNNHAAATATHGSGVIGGFGIGLSG	178
DB	61	SSISNGVHTVTESDGKSAISLCSFTSTLNNHAAATATHGSGVIGGFGIGLSG	120
QY	179	FDVVSFGIGRAMPFSTVGTATTNVSGNGHAAVPMATQFGLBSNAGGFVSGEYF	238
DB	121	FDVVSFGIGRAMPFSTVGTATTNVSGNGHAAVPMATQFGLBSNAGGFVSGEYF	180
QY	239	AMPDLSTTPGNSLK 253	
DB	181	AMPDLSTTPGNSLK 195	

RESULT 2

E96517 hypothetical protein F16N3.5 [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C:Accession: E96517
R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federpiel, N.A.; Kaul, S.; White, O.; Alonso,
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Creasy, T.H.; Dewar, K.;
ansen, N.F.; Hughes, B.; Huizart, L.
Nature 408, 816-820, 2000
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.

C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Lueros, J.S.; Maiti, R.; Marziani, R.; Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
 A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, Keri, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
 A:Title: Sequence and analysis of chromosome 1 of the plant *Arabidopsis*.
 A:Reference number: A66141; MUID:21016719; PMID:11130712
 A:Accession: E96517
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-209 <STO>
 A:Cross-references: UNIPROT:Q9SX97; GB:AE005173; NID:95668794; PIDN:AD46020.1; GSPDB:GN C:Genetics:
 A:Gene: F16N3.5
 A:Map position: 1

Query Match 29.5%; Score 402; DB 2; Length 209;
 Best Local Similarity 39.0%; Pred. No. 3e-22;
 Matches 101; Conservative 35; Mismatches 67; Indels 56; Gaps 13;

QY 1 MPTSDGEPRIAMKPNGVTPISDQEQLPCCPRCDSSNTKFCYNNYNFSGPRHPCAC 60
 D 1 MP-SEPNOTRPTROPSTRAAPRNLAEPPLCPRCNSTTTFCTYNNYNLAOPRYCKSC 59
 QY 61 RRYWTHGCTLRDVPVGGGTRK-SAKRSRTCSN--SSSSSVGVVNSNGVPLQTPVLPF 117
 D 60 RRYWTHGCTLRDVPVGGGTRSSSKRHRSFSTATSSSSSVITTTQEPATTEA---S 116
 QY 118 QSSISNGVTHVTESDQKGSALSCGFTSTLLHNAATAATHSGSVIGIG--FGIGL 175
 D 117 QTKVTHNIS-----GHGSFASLLGL-----GSGN---GGADYFGY 149
 QY 176 GSGFDVPSFG-IGRAMPFSTVGTATTNVGSGHHAVPMATWQEGLESNAGGPFVS 234
 D 150 GYGLBMSIGVLGD-----SSVGEIPV--VDGCGD-----TWQGEIDGKSG----- 190
 QY 235 GEYFAMPDLSTITPNSLX 253
 D 191 GDSLIWPGLRISMQTNIVK 209

RESULT 3

T52045
 Dof zinc finger protein [imported] - *Arabidopsis thaliana*
 C/Species: *Arabidopsis thaliana* (mouse-ear cress)
 C/Date: 20-Oct-2000 #sequence_revision 20-Oct-2000 #text_change 09-Jul-2004
 C/Accession: T52045
 R:Itagaki, T.; Kisu, Y.; Esaka, M.
 A:Submitted to the EMBL Data Library, September 1998
 A:Description: cDNA cloning and gene expression of Dof zinc finger protein in *Arabidopsis*.
 A:Reference number: 225919
 A:Accession: T52045
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-204 <ITR>
 A:Cross-references: UNIPROT:O82156; EMBL:AB017565; PIDN:BAA33197.1
 C:Genetics:
 A:Gene: adof2

Query Match 27.7%; Score 377.5; DB 2; Length 204;
 Best Local Similarity 48.8%; Pred. No. 1.8e-20;
 Matches 83; Conservative 21; Mismatches 43; Indels 23; Gaps 5;
 QY 26 QOEOLPCPRCDSSNTKFCYNNYNFSGPRHPCACRRTWTHGTLRDVPVGGGTRKSAKR 85
 D 25 EQEOLKCPKCDSPPTKFCYNNYNLSQPRHPCSKCRRTWTHGALRNVPVGGGSKKATK 84
 QY 86 SRTCSNSSSSSVGVNSNGVPLQTPVLPPOSISNGVTH-----VTESDGKGA 138
 D 85 RSTSSSSASAPSN--SQNKTKKPPDDPDRNSQKPDLDPTMLYGFPIGDQDVG-- 140
 QY 139 LSLCGSTSTLLHNAATAATHSGSVIGIGFGL-GSGFDVPSFGIG 187
 D 141 MEIGGSFSSLLANN-----MQLGIGGGGIMLDGSGMDHPGMGLG 179

RESULT 4

T02046
 prolamin box binding factor - maize
 C/Species: *Zea mays* (maize)
 C/Date: 26-Feb-1999 #sequence_revision 26-Feb-1999 #text_change 09-Jul-2004
 C/Accession: T02046
 R:Vicente-Carbalosa, J.; Moose, S.P.; Parsons, R.L.; Schmidt, R.J.
 A:Title: A maize zinc-finger protein binds the prolamin box in zein gene promoters and its
 A:Reference number: Z14511; MUID:97352860; PMID:9207153
 A:Accession: T02046
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-328 <VIC>
 A:Cross-references: UNIPROT:O24463; EMBL:U82230; NID:92393774; PIDN:AB70119.1; PID:9239
 C:Genetics:
 A:Gene: PBF

Query Match 24.0%; Score 327; DB 2; Length 328;
 Best Local Similarity 34.1%; Pred. No. 1.3e-16;
 Matches 88; Conservative 31; Mismatches 65; Indels 74; Gaps 9;

QY 5 DSGEPRIAMKPNGVTPISDQEQLPCCPRCDSSNTKFCYNNYNFSGPRHPCAC 60
 D 31 EARDPKOTRAMPQIGSGGERKRPQLPEALKCPKCDSSNTKFCYNNYNFSGPRHPCAC 90
 QY 61 RRYWTHGCTLRDVPVGGGTRKSAKR-----TCSNSSS---SVGVVNSN----- 105
 D 91 RRYWTHGCTLRNVPVGGGCKRKNHGRFVLGSHSSSSATVAPLSPSTVASSNSINK 150
 QY 106 -----GVPDLTTPPLFPQSSISNGVTHVTESDQKGSALSCGFTSTLLHNAAT 157
 D 151 HMMVPMWMTPTTNGLPF-----NVLEPTLPFGG-----GCFDTMDQHSLS 197
 QY 158 AT-----HSGSGSVIGGF-----GIGLGSFGDVPSFGIGRAMPFSTVGT 199
 D 198 FTPLMSLPQGPVPMVLAAGSEATPFLMLRGIFPGS-----SSVNTS 241
 QY 200 TTTNVGSGHHAVPM 217
 D 242 LTVSGGNGMDKPSLPS 259

RESULT 5

S59852
 DNA-binding protein Dof2 - maize (fragment)
 C/Species: *Zea mays* (maize)
 C/Date: 15-Feb-1996 #sequence_revision 01-Mar-1996 #text_change 09-Jul-2004
 C/Accession: S59852; S59850
 R:Shuichi, Y.
 A:Submitted to the EMBL Data Library, June 1994
 A:Reference number: S59852
 A:Accession: S59852
 A:Molecule type: mRNA
 A:Residues: 1-225 <SHU>
 A:Cross-references: UNIPROT:Q41800; EMBL:X79934; NID:91061305; PIDN:CA56287.1; PID:91061
 R:Yanagisawa, S.
 A:Nucleic Acids Res. 23, 3403-3410, 1995
 A:Title: A novel DNA-binding domain that may form a single zinc finger motif.
 A:Reference number: S59850; MUID:96032831; PMID:7567449
 A:Accession: S59850
 A:Status: nucleic acid sequence not shown
 A:Molecule type: mRNA
 A:Residues: 13-85/96-119/211-225 <YAN>
 A:Cross-references: EMBL:X79934
 C:Keywords: zinc finger

Query Match 23.5%; Score 320.5; DB 2; Length 225;
 Best Local Similarity 31.0%; Pred. No. 2.7e-16;
 Matches 80; Conservative 37; Mismatches 80; Indels 61; Gaps 8;

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 3, 2005, 16:08:45 ; Search time 60 Seconds
(without alignments)
2159.267 Million cell updates/sec

Title: US-10-509-691-2

Perfect score: 1363
Sequence: 1 MPTSDSGEPRIAMKPNQVT.....SGEYFAMPDLSTTPGNSLK 253

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : UniProt 03.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1363	100.0	253	1	DP34_ARATH
2	651	47.8	225	1	DP58_ARATH
3	600.5	44.1	234	2	Q76KU9
4	402	29.5	209	1	DP16_ARATH
5	377.5	27.7	204	1	DP31_ARATH
6	340	24.9	290	2	Q76KV1
7	338.5	24.8	324	2	Q9M4G1
8	336.5	24.7	396	2	Q76KV0
9	329	24.1	333	2	Q9ZS77
10	328	24.1	360	2	Q7XS99
11	328	24.1	378	2	Q9SXG8
12	327	24.0	328	1	PBF_MAIIZE
13	325.5	23.9	366	2	Q6EPG2
14	325.5	23.9	375	2	Q9SXG7
15	322	23.6	371	2	Q6F2W0
16	321.5	23.6	330	2	Q8L5B9
17	321.5	23.6	330	2	Q6RK62
18	321.5	23.6	330	2	Q9ZRX2
19	321.5	23.6	355	2	Q84T97
20	320.5	23.5	225	2	Q41800
21	320.5	23.5	307	1	DP54_ARATH
22	320	23.5	372	1	DP56_ARATH
23	318	23.3	194	1	DP17_ARATH
24	317.5	23.3	331	2	Q6ICV3
25	317.5	23.3	399	1	DP51_ARATH
26	317	23.3	359	1	Q8LIJ0
27	316.5	23.2	331	1	DP11_ARATH
28	316	23.2	241	2	Q76KV7
29	315	23.1	332	2	Q7X170
30	314.5	23.1	262	2	Q82027
31	314.5	23.1	296	2	Q76KV2

32	313.5	23.0	290	2	Q65XV0	Q65XV0 oryza sativ
33	312.5	22.9	311	1	DP14_ARATH	Q9FZ44 arabidopsis
34	312	22.9	276	2	Q6ZB01	Q6ZB01 oryza sativ
35	311.5	22.9	340	1	DP22_ARATH	Q9ZV33 arabidopsis
36	309	22.6	352	1	DP18_ARATH	Q84JQ8 arabidopsis
37	308.5	22.6	234	2	Q43570	Q43570 nicotiana t
38	308.5	22.6	472	2	Q8RVK0	Q8RVK0 hordeum vul
39	308.5	22.6	472	2	Q8RVK1	Q8RVK1 hordeum vul
40	308	22.6	369	1	DP25_ARATH	Q9ZPY0 arabidopsis
41	306.5	22.5	257	1	DP53_ARATH	Q84E98 arabidopsis
42	305	22.4	245	1	DP32_ARATH	Q9M166 arabidopsis
43	304	22.3	288	1	DP21_ARATH	Q81E43 arabidopsis
44	303.5	22.3	282	2	Q6Z3F5	Q6Z3F5 oryza sativ
45	303.5	22.3	282	2	Q9SXG5	Q9SXG5 oryza sativ

ALIGNMENTS

RESULT 1
DP34_ARATH STANDARD; PRT; 253 AA.
ID DP34_ARATH
AC Q93088; Q9M2R8;
DT 25-OCT-2004 (Rel. 45, Created)
DT 25-OCT-2004 (Rel. 45, Last sequence update)
DT 25-JAN-2005 (Rel. 46, Last annotation update)
DE DoF zinc finger protein DOF3.4 (AtDOF3.4) (OBF binding protein 1).
GN Name=DOF3.4; Synonyms=OBP1; OrderedLocNames=At3g50410;
GN ORFNames=P11C1.250;
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurossids II; Brassicales; Brassicaceae; Arabidopsi.
OX NCBI_TaxID=3702;
RX [1]
RN SEQUENCE FROM N.A., TISSUE SPECIFICITY, AND INTERACTION WITH OBP4 AND
RP OBP5.
RC STRAIN=cv. Columbia;
RX Zhang B., Chen W., Foley R.C., Buettner M., Singh K.B.;
RA MEDLINE=96351937; PubMed=8718629;
RT "Interactions between distinct types of DNA binding proteins enhances
binding to ocs-element promoter sequences";
RL Plant Cell 7:2241-2252(1995).
[2]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Columbia;
RX MEDLINE=21016720; PubMed=11130713; DOI=10.1038/35048706;
RA Salanoubat M., Lemcke K., Rieger M., Ansgore W., Unseld M.,
RA Fattmann B., Valle G., Bloeker H., Perez-Alonso M., Obermayer B.,
RA Delseny M., Boutry M., Grivell L.A., Maché R., Puigdomenech P.,
RA De Simone V., Cholene N., Artiguenave F., Robert C., Brottier P.,
RA Wincker P., Catalicio L., Weissenbach J., Saurin W., Quetier F.,
RA Schaefer M., Mueller-Auer S., Gabel C., Fuchs M., Benes V.,
RA Wumbsch E., Drzonek H., Erfle H., Jordan N., Bangert S.,
RA Widelmann R., Kranz H., Voss H., Holland R., Brandt P., Nyakatura G.,
RA Verzi A., D'Angelo M., Pallavicini A., Toppo S., Simionati B.,
RA Conrad A., Hornischer K., Kauer G., Loenert T.-H., Nordiek G.,
RA Reichelt J., Scharfe M., Schoen O., Baynes M., Terol J., Climent J.,
RA Navarro P., Collado C., Perez-Perez A., Ottenwaelder B., Duchemin D.,
RA Cooke R., Iandje M., Berger-Liauro C., Purnelle B., Masuy D.,
RA de Haan M., Maare A.C., Alcaraz J.-P., Cottet A., Casacuberta E.,
RA Monfort A., Argitlou A., Flores M., Lignori R., Vitale D.,
RA Mannheim G., Haase D., Schoof H., Rudd S., Zaccaria P., Mewes H.-W.,
RA Mayer K.F.X., Kaul S., Town C.D., Koo H.L., Talon L.J., Jenkins J.,
RA Rooney T., Rizzo M., Walts A., Uteback T., Fujii C.Y., Shea T.P.,
RA Creaey T.H., Haas B., Walts R., Wu D., Peterson J., Van Aken S.,
RA Pal G., Miltischer J., Sellers P., Gill J.E., Feldlyum T.V.,
RA Pruss D., Lin X., Nieman W.C., Salzberg S.L., White O., Venter J.C.,
RA Fraser C.M., Kaneko T., Nakamura Y., Sato S., Kato T., Asamizu E.,
RA Sasamoto S., Kimura T., Idegawa K., Kawashima K., Kishida Y.,
RA Kiyokawa C., Kohara M., Matsumoto M., Matsumoto M., Mutaki A.,
RA Nakayama S., Nakazaki N., Shino S., Takeuchi C., Wada T.,
RA Watanabe A., Yamada M., Yasuda M., Tabata S.;

```

RT "Sequence and analysis of chromosome 3 of the plant Arabidopsis
RT thaliana."
RL Nature 408:820-822(2000).
RN (3)
RP TISSUE SPECIFICITY, AND INDUCTION.
RX PubMed=10758484;
RA Kang H.-G., Singh K.B.;
RT "Characterization of salicylic acid-responsive, Arabidopsis Dof domain
RT proteins: overexpression of OBP3 leads to growth defects."
RL Plant J. 21:329-339(2000).
RN (4)
RP GENE FAMILY, AND NOMENCLATURE.
RX PubMed=12475498;
RA Yanagisawa S.;
RT "The Dof family of plant transcription factors."
RL Trends Plant Sci. 7:555-560(2002).
CC -1- FUNCTION: Transcription factor that binds specifically to a 5'-
CC AA[AG]G-3' consensus core sequence. Enhances the DNA binding of
CC OBP transcription factors to OCS elements.
CC -1- SUBUNIT: Interacts with OBP4 or OBP5.
CC -1- SUBCELLULAR LOCATION: Nuclear (Probable).
CC -1- TISSUE SPECIFICITY: Constitutively expressed in the whole plant.
CC -1- INDUCTION: By auxin and salicylic acid (SA).
CC -1- SIMILARITY: Contains 1 Dof-type zinc finger.
CC -1- CAUTION: Ref.1 sequence differs from that shown due to a
CC frameshift in position 4.
CC -----
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CC -----
DR EMBL: X89192; CAAG1485.1; ALT_FRAME.
DR EMBL: ALJ32976; CAB88324.1; -.
DR PIR: T46072; T46072.
DR TRASNFA: T02694; -.
DR InterPro: IPR003851; Znf_Dof.
DR Pfam: PF02701; ZF-Dof; 1.
DR PROSITE: PS01361; ZF_DOF_1; 1.
DR PROSITE: PS50884; ZF_DOF_2; 1.
KW DNA-binding; Metal-binding; Nuclear protein; Trans-acting factor;
KW Transcription regulation; Zinc; Zinc-finger.
FT ZN_FING 30 84 Dof-type.
FT DOMAIN 90 98 Poly-Ser.
FT CONFLICT 155 155 A->R (in Ref. 1).
SQ SEQUENCE 253 AA; 26382 MW; 3A64EA3FECF0A5D1 CRC64;
Query Match 100.0%; Score 1363; DB 1; Length 253;
Best Local Similarity 100.0%; Pred. No. 5.5e-93;
Matches 253; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MPTSDSEPRRIAKKPVGVPIISDQEQLPFCPCDSSNTKFCYNNYNSQPRHFKAC 60
DB 1 MPTSDSEPRRIAKKPVGVPIISDQEQLPFCPCDSSNTKFCYNNYNSQPRHFKAC 60
QY 61 RRYVTHGTLRDVVGCGTRKSAKRSRTCSNSSSSSVGVVNSNGVPLQTTPLVFPQSS 120
DB 61 RRYVTHGTLRDVVGCGTRKSAKRSRTCSNSSSSSVGVVNSNGVPLQTTPLVFPQSS 120
QY 61 RRYVTHGTLRDVVGCGTRKSAKRSRTCSNSSSSSVGVVNSNGVPLQTTPLVFPQSS 120
DB 61 RRYVTHGTLRDVVGCGTRKSAKRSRTCSNSSSSSVGVVNSNGVPLQTTPLVFPQSS 120
QY 121 ISNGVTHVTESDGKSLICGSFTSTLLNHNAAATATHGSGSVIGGFGIGLGSQFD 180
DB 121 ISNGVTHVTESDGKSLICGSFTSTLLNHNAAATATHGSGSVIGGFGIGLGSQFD 180
QY 121 ISNGVTHVTESDGKSLICGSFTSTLLNHNAAATATHGSGSVIGGFGIGLGSQFD 180
DB 121 ISNGVTHVTESDGKSLICGSFTSTLLNHNAAATATHGSGSVIGGFGIGLGSQFD 180
QY 181 DVSGGLGRAMPFSTVGTATTTNGSNGCHRAVPMPTWQEGLESNAGGFPVSGEYFAW 240
DB 181 DVSGGLGRAMPFSTVGTATTTNGSNGCHRAVPMPTWQEGLESNAGGFPVSGEYFAW 240
QY 241 PDLSITTPGNSLK 253
DB 241 PDLSITTPGNSLK 253
QY 241 PDLSITTPGNSLK 253
DB 241 PDLSITTPGNSLK 253

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RESULT 2
ID DPF8_ARATH STANDARD; PRT; 225 AA.
AC QPRGDE;
DT 25-JAN-2005 (Rel. 46, Created)
DT 25-JAN-2005 (Rel. 46, Last sequence update)
DT 25-JAN-2005 (Rel. 46, Last annotation update)
DE Hypothetical Dof zinc finger protein DPF8 (AtDPF8.8).
GN Name=DPF8.8; OrderedLocustNames=At5G66940; ORFNames=KRA10.1;
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eustosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Columbia;
RA Kaneke T., Katoh T., Asamizu E., Sato S., Nakamura Y., Kotani H.,
RA Tabata S.;
RT "Structural analysis of Arabidopsis thaliana chromosome 5. XI."
RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP GENE FAMILY, AND NOMENCLATURE.
RX PubMed=12475498;
RA Yanagisawa S.;
RT "The Dof family of plant transcription factors."
RL Trends Plant Sci. 7:555-560(2002).
CC -1- FUNCTION: Transcription factor that binds specifically to a 5'-
CC AA[AG]G-3' consensus core sequence (By similarity).
CC -1- SUBCELLULAR LOCATION: Nuclear (Probable).
CC -1- SIMILARITY: Contains 1 Dof-type zinc finger.
CC -----
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CC -----
DR EMBL: AB026640; BAB08933.1; -.
DR InterPro: IPR003851; Znf_Dof.
DR Pfam: PF02701; ZF-Dof; 1.
DR PROSITE: PS01361; ZF_DOF_1; 1.
DR PROSITE: PS50884; ZF_DOF_2; 1.
KW DNA-binding; Hypothetical protein; Metal-binding; Nuclear protein;
KW Trans-acting factor; Transcription regulation; Zinc; Zinc-finger.
FT ZN_FING 32 86 Dof-type.
SQ SEQUENCE 225 AA; 24117 MW; 313D80AC406FC09D CRC64;
Query Match 47.8%; Score 651; DB 1; Length 225;
Best Local Similarity 55.5%; Pred. No. 2e-40;
Matches 137; Conservative 31; Mismatches 49; Indels 30; Gaps 10;
QY 1 MPTSDSEPRRIAKKPVGVPIISDQEQLPFCPCDSSNTKFCYNNYNSQPRHFKAC 56
DB 1 MPTSDSEPRRIAKKPVGVPIISDQEQLPFCPCDSSNTKFCYNNYNSQPRHFKAC 56
QY 1 MPTSDSEPRRIAKKPVGVPIISDQEQLPFCPCDSSNTKFCYNNYNSQPRHFKAC 56
DB 1 MPTSDSEPRRIAKKPVGVPIISDQEQLPFCPCDSSNTKFCYNNYNSQPRHFKAC 56
QY 57 CKAKRRYTHGTLRDVVGCGTRKSAKRSRTCSNSSSSSVGVVNSNGVPLQTTPLV 116
DB 57 CKAKRRYTHGTLRDVVGCGTRKSAKRSRTCSNSSSSSVGVVNSNGVPLQTTPLV 116
QY 57 CKAKRRYTHGTLRDVVGCGTRKSAKRSRTCSNSSSSSVGVVNSNGVPLQTTPLV 116
DB 57 CKAKRRYTHGTLRDVVGCGTRKSAKRSRTCSNSSSSSVGVVNSNGVPLQTTPLV 116
QY 117 POSSISNGVTHVTESDGKSLICGSFTSTLLNHNAAATATHGSGSVIGGFGIGL 176
DB 117 POSSISNGVTHVTESDGKSLICGSFTSTLLNHNAAATATHGSGSVIGGFGIGL 176
QY 117 POSSISNGVTHVTESDGKSLICGSFTSTLLNHNAAATATHGSGSVIGGFGIGL 176
DB 117 POSSISNGVTHVTESDGKSLICGSFTSTLLNHNAAATATHGSGSVIGGFGIGL 176
QY 177 SG--FDVSGFLGRAMPFSTVGT--ATTNVSNGCHRAVPMPTWQEGLESNAGG 232
DB 177 SG--FDVSGFLGRAMPFSTVGT--ATTNVSNGCHRAVPMPTWQEGLESNAGG 232
QY 168 HGSYEDVRVGGGIGITVWPFSSGATDAATTS-----HIAQIPATWQEGGSSKV--GF 218
DB 168 HGSYEDVRVGGGIGITVWPFSSGATDAATTS-----HIAQIPATWQEGGSSKV--GF 218
QY 233 VSGEYFA 239
DB 233 VSGEYFA 239

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Db 219 VSGDYVA 225

RESULT 3

076KU9 PRELIMINARY; PRT; 234 AA.

DT 05-JUL-2004 (TREMBLrel. 27, Created)
 DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
 DE DNA binding with one finger 5 protein.
 GN Name=PsdoF5;
 OS Pisum sativum (Garden pea).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC Eucosida 1; Fabales; Fabaceae; Papilionoideae; Viciaeae; Pisum.
 OC NCBI_TaxID=3888;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Epilcotyle;
 RA Nakamura N., Marutani M., Senematsu S., Toyoda K., Inagaki Y.-S.,
 RA Shiraishi T., Ichinose Y.,
 RT "Phylogenetic Classification of DoF-type Transcription Factors in Pea
 (Pisum sativum).";
 RL Plant Biotechnol. 20:247-253(2003).
 DR EMBL: AB087850; BAC81662.1;
 DR GO: GO:0003677; P:DNA binding; IEA.
 DR InterPro: IPR003851; Znf_Dof.
 DR Pfam: PF02701; zF_Dof; 1.
 DR PROSITE: PS01361; ZF_DOF_1; UNKNOWN_1.
 DR PROSITE: PS50884; ZF_DOF_2; 1.
 SQ SEQUENCE 234 AA; 24607 MW; C28B6801EBE7370B CRC64;

Query Match 44.1%; Score 600.5; DB 2; Length 234;
 Best Local Similarity 50.8%; Pred. No. 1.1e-36;
 Matches 134; Conservative 32; Mismatches 57; Indels 41; Gaps 13;

QY 1 MPTSGSEPRRIAMENGVTVPISDQOQLPCPRCDSSNTKFCYNNNTNFSPRRHCRAC 60
 Db 1 MPSSSGSSSR-SIKPQNPGAPAPBQENLPCCPRCDSTTKFCYNNNTNFSPRRHCRAC 59
 QY 61 RRYWTHGGLTDVDPVGGGTRKSAKRSRT--CSNSSSSSVGVNSNGVPLQTTVPVLPFQ 118
 Db 60 RRYWTHGGLTDVDPVGGGTRKSAKRSRTTHAVTSSSSSAVTS--APQNTYSMPRI 115
 QY 119 SSIS--NGVTHVTESDQKGA-LSLCGSFTSTLLNNAATAATHGSGVIGGFGIG 174
 Db 116 QGGSPPYGGV-----DQEGKQNNSSVCGSFTS-LLNNN-----PQNSGFLALGGFGIG 162
 QY 175 LGSFDDVSPGLGRAMPSTVGTATTNVTGNSNGHHAVPMPA-----TWQFEGLESNAG 229
 Db 163 LGHGIGDGGFGIGRE-WSPF--GMMDGSNMG-----VPVSSGSGNSGMOLEGGETGV 212
 QY 230 GGFVSGEYFAMPDLITTPGNSLX 253
 Db 213 GG--GGDCTSWPGLAISTFGNLX 234

RESULT 4
 DP16 ARATH
 AC 096557;
 ID DP16 ARATH STANDARD; PRT; 209 AA.

DT 25-JAN-2005 (Rel. 46, Created)
 DT 25-JAN-2005 (Rel. 46, Last sequence update)
 DE Hypothetical DoF zinc finger protein DOF1.6 (AtDOF1.6).
 GN Name=DOF1.6; OrderedlocusNames=At1g94765; ORFNames=FLN3.5;
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC Eucosida 1; Brassicales; Brassicaceae; Arabidopsids.
 OC NCBI_TaxID=3702;

RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Columbia;
 RX MEDLINE=21016719; PubMed=11130712; DOI=10.1038/35048500;
 RA Theologis A., Ecker J.R., Palm C.J., Federspiel N.A., Kaul S.,
 RA White O., Alonso J., Altieri H., Araujo R., Bowman C.L., Brooks S.Y.,
 RA Buehler E., Chan A., Chao Q., Chen H., Cheuk R.F., Chin C.W.,
 RA Chung M.K., Conn L., Conway A.B., Cressy T.H., Dewar K.,
 RA Dunn P., Egu P., Feldblyum T.V., Feng U.-D., Fong B., Fujii C.Y.,
 RA Gill J.E., Goldsmith A.D., Haas B., Hansen N.F., Hughes B., Hultzer L.,
 RA Hunter J.L., Jenkins J., Johnson-Hopson C., Khan S., Khaykin E.,
 RA Kim C.J., Koo H.L., Kremetska I., Kurtz D.B., Kwan A., Lam B.,
 RA Langin-Hooper S., Lee A., Lee J.M., Lenz C.A., Li J.H., Li Y.-P.,
 RA Lin X., Liu S.X., Liu Z.A., Iwros J.S., Maiti R., Marziani A.,
 RA Millican J., Miranda M., Nguyen M., Niernan W.C., Osborne B.I.,
 RA Pal G., Peterson J., Pham P.K., Rizzo M., Rooney T., Rowley D.,
 RA Sakano H., Salzberg S.L., Schwartz J.R., Shinn P., Southwick A.M.,
 RA Sun H., Tallon L.J., Tambunga G., Toriumi M.J., Town C.D.,
 RA Utecherback T., Van Aken S., Vayberg M., Vysotskaia V.S., Walker M.,
 RA Wu D., Yu G., Fraser C.M., Venter J.C., Davis R.W.;
 RT "Sequence and analysis of chromosome 1 of the plant Arabidopsis
 thaliana.";
 RL Nature 408:816-820(2000).
 RN [2]
 RP GENE FAMILY, AND NOMENCLATURE.
 RX PubMed=12475498;
 RA Yanagiawa S.;
 RT "The DoF family of plant transcription factors.";
 RL Trends Plant Sci. 7:555-560(2002).
 CC -I- FUNCTION: Transcription factor that binds specifically to a 5'-
 AALAGG-3' consensus core sequence (By similarity).
 CC -I- CELLULAR LOCATION: Nuclear (Probable).
 CC -I- SIMILARITY: Contains 1 DoF-type zinc finger.

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CC EMBL: AC007519; AAC46020.1; -
 DR PIR: E96517; E96517.
 DR InterPro: IPR003851; Znf_Dof.
 DR Pfam: PF02701; zF_Dof; 1.
 DR PROSITE: PS01361; ZF_DOF_1; 1.
 DR PROSITE: PS50884; ZF_DOF_2; 1.
 KW DNA-binding; Hypothetical protein; Metal-binding; Nuclear protein;
 KW Trans-acting factor; Transcription regulation; Zinc; Zinc-finger.
 FT ZN_FING 29
 FT DOMAIN 81
 FT DOMAIN 101
 FT DOMAIN 126
 FT DOMAIN 191
 SQ SEQUENCE 209 AA; 22292 MW; 0BC93B44C49F09E CRC64;

Query Match 29.5%; Score 402; DB 1; Length 209;
 Best Local Similarity 39.0%; Pred. No. 4.8e-22;
 Matches 101; Conservative 35; Mismatches 67; Indels 56; Gaps 13;

QY 1 MPTSGSEPRRIAMENGVTVPISDQOQLPCPRCDSSNTKFCYNNNTNFSPRRHCRAC 60
 Db 1 MP-SEPNQRTPRVGPSTAAVPPVLAAPLPBPCPRCNSITTKFCYNNNTNLAQPRYYCSC 59
 QY 61 RRYWTHGGLTDVDPVGGGTRK-SAKRSRTCSN--SSSSSVGVNSNGVPLQTTVPVLPF 117
 Db 60 RRYWTHGGLTDVDPVGGGTRSSSKRRSFTTATSSSSSSSVITTTQEPATTA---S 116
 QY 118 OSSISNGVTHVTESDQKGSALSLCGSFTSTLLNNAATAATHGSGVIGG--FGIGL 175
 Db 117 QTKVNLIS-----GGGSFASLIGL-----GSGN-----GGLDYGRGY 149
 QY 176 GSGFDDVSPG-LGRAMPSTVGTATTNVTGNSNGHHAVPMPATVQFEGLESNAGGGRVS 234

```

Db 150 GYGELEMSIGYLGD-----SSVGEIPV--VDGCGD-----TWIGIEBKGSG----- 190
Qy 235 GEFYAMPDLSTTPGNSLK 253
Db 191 GDSLWPGLEISMQRNDYK 209

RESULT 5
ID DF31 ARATH STANDARD; PRT; 204 AA.
AC 094AR6; 082156;
DT 25-OCT-2004 (Rel. 45, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last sequence update)
DT 25-JAN-2005 (Rel. 46, Last annotation update)
DE Dof zinc finger protein DOF3.1 (AtDOF3.1).
GN Name=DOF3.1; Synonyms=ADOZF; OrderedLocustNames=At3g21270;
OS ORFNames=MXL8.14;
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Seedling;
RA Itagaki T., Kisu Y., Saaka M.;
RT "cDNA cloning and gene expression of Dof zinc finger protein in
RT Arabidopsis thaliana.";
RN Submitted (SEP-1998) to the EMBL/Genbank/DBJ databases.
[2]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Columbia;
RA MEDLINE=20277480; PubMed=10819329;
RA Sato S., Nakamura Y., Kaneko T., Asamizu E., Tabata S.;
RT "Structural analysis of Arabidopsis thaliana chromosome 3. I. Sequence
RT features of the regions of 4,504,864 bp covered by sixty pl and TAC
RT clones.";
RN DNA Res. 7:131-135(2000).
[3]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Columbia;
RX MEDLINE=22954850; PubMed=14593172; DOI=10.1126/science.1088105;
RA Yamada K., Lim Y., Dale J.M., Chen H., Shim P., Palm C.J.,
RA Southwick A.M., Wu H.C., Kim C.J., Nguyen M., Pham P.K., Cheuk R.F.,
RA Karlin-Newmann G., Liu S.X., Lam B., Sakano H., Wu T., Yu G.,
RA Miranda M., Quach H.L., Tripp M., Chang C.H., Lee J.M., Toriumi M.J.,
RA Chan M.M., Tang C.C., Onodera C.S., Deng J.M., Akiyama K., Anzari Y.,
RA Arakawa T., Banh J., Banno F., Bowser L., Brooks S.Y., Carninci P.,
RA Chao Q., Choy N., Ejiri A., Goldsmith A.D., Gurjal M., Hansen N.F.,
RA Hayashizaki Y., Johnson-Hopson C., Hsuan V.W., Iida K., Karnes M.,
RA Khan S., Koeseema E., Ishida J., Jiang P.X., Jones T., Kawai J.,
RA Kamiya A., Meyers C., Nakajima M., Narusaka M., Seki M., Sakurai T.,
RA Satou M., Tamme R., Vaysberg M., Wallender E.K., Wong C., Yamamura Y.,
RA Yuan S., Shinozaki K., Davis R.W., Theologis A., Ecker J.R.;
RT "Empirical analysis of transcriptional activity in the Arabidopsis
RT genome.";
RN Science 302:842-846(2003).
[4]
RN GENE FAMILY, AND NOMENCLATURE.
RP PubMed=12475498;
RX Yanagisawa S.;
RA "The Dof family of plant transcription factors.";
RT Trends Plant Sci. 7:555-560(2002).
CC -1- FUNCTION: Transcription factor that binds specifically to a 5'-
CC AAGAGG-3' consensus core sequence (By similarity).
CC -1- SUBCELLULAR LOCATION: Nuclear (Probable).
CC -1- SIMILARITY: Contains 1 Dof-type zinc finger.
CC -----
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CC -----
DR EMBL; AB017565; BAA33197.1; -
DR EMBL; AB023045; BAB01720.1; -
DR EMBL; AY045847; AAK76521.1; -
DR EMBL; AY150391; AAN12936.1; -
DR PIR; T52045; T52045.
DR InterPro; IPR003851; ZnF_Dof.
DR Pfam; PF02701; 2f-Dof; 1.
DR PROSITE; PS01361; ZF_DOF_1; 1.
DR PROSITE; PS00884; ZF_DOF_2; 1.
KW DNA-binding; Metal-binding; Nuclear protein; Trans-acting factor;
KW Transcription regulation; Zinc; Zinc-finger.
FT ZN FING 29
FT CONFLICT 97 97 S->T (in Ref. 3; AAK76521).
SQ SEQUENCE 204 AA; 22530 MW; 4D6FEPD4BCS1759 CRC64;

Query Match 27.7%; Score 377.5; DB 1; Length 204;
Best Local Similarity 48.8%; Pred. No. 3e-20;
Matches 83; Conservative 21; Mismatches 43; Indels 23; Gaps 5;

Qy 26 QOEOLPCCRDSSNTKCYNNYVFSQPRHFCACRRTWTHGTLRDVPVGGGTRKSAKR 85
Db 25 EQEOQKCPDCDSPTKFCYNNYVMSQPRHFCCKRCRYWTKGALRVNVPVGGGSRKNATK 84

Qy 86 SRTCSNSSSSVSGVNSNGVPLQTTPLVPEPSSISNGVTHT-----VTESDGKSA 138
Db 85 RSTSSSSSSASPSN--SSQKKTGNPPDPDPFRNSQRPDLPTMLYGFPGDDPVKG-- 140

Qy 139 LSLGFSFTSLNLNNAATATHSGSVIGIGFGIGL-GSGFDDVSFGLG 187
Db 141 MEIGSGFSSTLANN-----MQLGLGGGIGMLDGGMDHPGMLG 179

RESULT 6
Q76KV1 PRELIMINARY; PRT; 290 AA.
AC Q76KV1;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE DNA binding with one finger 3 protein.
GN Name=PSDOF3;
OS Pisum sativum (Garden pea).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids I; Fabales; Fabaceae; Papilionoideae; Viciaeae; Pisum.
OX NCBI_TaxID=3888;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Epicytyle;
RA Nakamura N., Marutani M., Sanematsu S., Toyoda K., Inagaki Y.-S.,
RA Shirahashi T., Ichinose Y.;
RT "Phylogenetic Classification of Dof-type Transcription Factors in Pea
RT (Pisum sativum).";
RN Plant Biotechnol. 20:247-253(2003).
RT EMBL; AB087848; BAC81600.1; -
DR GO; GO:0003577; F-DNA binding; IEA.
DR InterPro; IPR003851; ZnF_Dof.
DR Pfam; PF02701; ZF_DOF_1.
DR PROSITE; PS01361; ZF_DOF_1; UNKNOWN_1.
DR PROSITE; PS00884; ZF_DOF_2; 1.
SQ SEQUENCE 290 AA; 31740 MW; 9637CF3508582DA CRC64;

Query Match 24.9%; Score 340; DB 2; Length 290;
Best Local Similarity 34.8%; Pred. No. 2.6e-17;
Matches 79; Conservative 40; Mismatches 94; Indels 14; Gaps 4;

Qy 26 QOEOLPCCRDSSNTKCYNNYVFSQPRHFCACRRTWTHGTLRDVPVGGGTRKSAKR 85
Db 17 QOQALCPKRDSSNTKCYNNYVLSQPRHFCACRRTWTHGTLRDVPVGGGTRKSNKR 76

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QY 86 SRTCSNSSSSVSGVSNNGVPLQTPVLPFOSSISNGVHTVTESD-----GKGSAL 139
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 77 SRTSSNGPSTSTTLTKR-----PISTIETATSNSSSPSTSSSTSNMNPFGYLSSTN 131
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 140 SLCG-SFTSTLNNHNAATATGSSVIGIGFGIGLGSFGDDVSF--GLGRAMPFSTV 196
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 132 NPCDNLPFSRFRNITSRLSTSSGYDLQPOMNFFGLFGSSGFENNNGYTNFNTSNNNYDSI 191
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 197 GATATTNNGSGHHAVPMPATWQFEGLESNAGGFVSGETVAMPDL 243
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 192 FSSSTISASNNITSVMPSSVLSSTLLQHKFFDDGLKYGSDAGSNGAFODL 238
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 7
Q9MAG1 PRELIMINARY; PRT; 324 AA.
ID Q9MAG1
AC Q9MAG1
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DR 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE Dof zinc finger protein.
GN Name=dof1;
OS Solanum tuberosum (Potato).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC Lamiales; Solanales; Solanaceae; Solanum.
OC NCBI_TaxID=4113;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Epidermal fragments;
RA Plesch G., Ehrhardt T., Mueller-Roeber B.;
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ242853; CAB69831.1; -.
DR TRANSFAC; T05500; -.
DR GO; GO:0003677; F:DNA binding; IEA.
DR InterPro; IPR003851; ZnF_Dof.
DR Pfam; PF02701; zf-Dof; 1.
DR PROSITE; PS01361; ZF_DOF_1; UNKNOWN_1.
DR PROSITE; PS50884; ZF_DOF_2; 1.
SQ SEQUENCE 324 AA; 35057 MW; 62E79B2214395C25 CRC64;

Query Match 24.8%; Score 338.5; DB 2; Length 324;
Best Local Similarity 33.0%; Pred. No. 3.8e-17;
Matches 93; Conservative 35; Mismatches 99; Indels 55; Gaps 13;

QY 9 PRRIAMKNGV-----TVPISDQEQLPCCPRCDSSNTFCYNNNTNBSQPRHF 56
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 40 PMOVGASPGSIRPGSMVDRARLAKIPL--PEAGLKCPRCDSTNTKFCYFNNTNLSQPRHF 97
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 57 CKACRRYTHGGTLRDVPGGSTRKAKRSRTCSNSSSSVSGVSNNGVPLQTPVLP 116
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 98 CKTCRRYTRGAGALSVPVGGGCRKN-KSKSNNNNNSSKTASGVNNTNTTASGTSTAS 156
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 117 PQS--SISNGVTHTVTESDGKSALSLCGSFTSTLLNNHNA-----TATGSGSVIG 167
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 157 PSSCSTEIMNGHHHSHQPRQ--LTPMAAFQN--LNNHVGFGQRPPLVSTHHNGTGA 212
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 168 IG-----GFGIGL-----GSGFDD---VSFGLGRAMPF---STVGTATTTNV 204
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 213 LGHHHEMFQIGSSNTNNTLPPVPGGSGSHQWRPLSLAANTNLVYFQHDGQIHSSSV 272
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 205 GSN--GHHAVMPATWQFEGLESNAGGFVSGETVAMPDL 244
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 273 NNNNNIADDOGLNTKQFLGMENTNTOYMGSN--ANTGFS 312
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 8
Q76KV0 PRELIMINARY; PRT; 396 AA.
ID Q76KV0
AC Q76KV0
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)

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DE DNA binding with one finger 4 protein.
GN Name=Padof4;
OS Pisum sativum (Garden pea).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eucosids I; Fabales; Fabaceae; Papilionoideae; Viciae; Pisum.
OC NCBI_TaxID=3888;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=epicotyls;
RA Nakamura N., Marutani M., Sanematsu S., Toyoda K., Inagaki Y.-S.,
RA Shiraishi T., Ichinose Y.;
RT "Phylogenetic Classification of Dof-type Transcription Factors in Pea
RT (Pisum sativum).";
DR EMBL; AB087849; BAC81661.1; -.
DR GO; GO:0003677; F:DNA binding; IEA.
DR InterPro; IPR003851; ZnF_Dof.
DR Pfam; PF02701; zf-Dof; 1.
DR PROSITE; PS01361; ZF_DOF_1; UNKNOWN_1.
DR PROSITE; PS50884; ZF_DOF_2; 1.
SQ SEQUENCE 396 AA; 43073 MW; 97DF573A5E86ED9F CRC64;

Query Match 24.7%; Score 336.5; DB 2; Length 396;
Best Local Similarity 31.0%; Pred. No. 6.6e-17;
Matches 98; Conservative 26; Mismatches 95; Indels 97; Gaps 11;

QY 6 SGEPRRIAMKNGVTPVPSDQEQQLPCPRCDSSNTFCYNNNTNBSQPRHF 65
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 35 SSTGNRVMEKPGQEL--LQOQOQALRCPCRSSNTKFCYNNNTSLQPRHFCKACKRYWT 92
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 66 HGGTLRDVPGGSTRKAKRSR---TGSNS-----SSSVSGVSNNGVPLQTP 113
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 93 RGGTLRNVVGGGCKKRLKPTVPCSNNNNIDPSASPSSTPSSVAVNPV-PSQSQO 151
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 114 VLFPOS--SISNGVTHTVTESDGKSALSLCGSFTSTLLNNHNAATATGSGSVIG 169
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 152 QQQQQQHHSFDIAATSNNTNMLYGCNSCHDVNMPFTRFRSTTRVNPASGVNLPQN 211
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 170 GFGIGLGSF-----DVVSFGLGRAMPFST-----VGATAT 201
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 212 GIGLGFSSGILMSAAGFVNLNHHNHHDGSGYRNG-----FSTSNNNVSSIGSSST 266
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 202 TN-----VGSNGG-----HHAVPRA----- 217
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 267 TTPVMASSLSTLLQOKWGTGGGIGKGGGGGDDDFPHHQEDSKVKLGSLQNR 326
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 218 -TWQFEGLESNAGGF 232
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 327 DQNNNNNNGNGAVF 342
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 9
Q9ZS77 PRELIMINARY; PRT; 333 AA.
ID Q9ZS77
AC Q9ZS77
DT 01-MAY-1999 (TREMBlrel. 10, Created)
DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE DNA binding protein.
GN Name=BBP;
OS Hordeum vulgare (Barley).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
OC Triticeae; Hordeum.
OC NCBI_TaxID=4513;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=99024959; PubMed=9807827;
RA Mena M., Vicente-Carabajosa J., Schmidt R.J., Carbonero P.;
RT "An endosperm-specific Dof protein from barley, highly conserved in
RT wheat, binds to and activates transcription from the prolamin-box of a
RT native B-hordein promoter in barley endosperm.";

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OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Erihartoideae; Oryzaceae; Oryza.
 OX NCBI_TaxID=4530;
 RN
 RP SEQUENCE FROM N.A.
 RC STRAIN=Yukihikari; TISSUE=Aleurone layer;
 RX MEDLINE=99418329; PubMed=10490396;
 RA Maehio K.;
 RT "cDNA encoding Dof-proteins that are present in germinated aleurone
 cells (Accession Nos. AB028129, AB028130, AB028131, AB028132, and
 AB028133). (FGR99-107)."
 RL Plant Physiol. 120:1205-1205(1999).
 DR EMBL; AB028130; BAA78573.1; -.
 DR TRANSFAC; T05290; -.
 DR Gramene; O95XG7; -.
 DR GO; GO:0003677; F:DNA binding; IEA.
 DR InterPro; IPR003851; Znf_Dof.
 DR Pfam; PF02701; Zf-Dof; 1.
 DR PROSITE; PS01361; ZF_DOF_1; UNKNOWN_1.
 DR PROSITE; PSS0884; ZF_DOF_2; 1.
 SQ SEQUENCE 375 AA; 3786 MW; FEC8A020780EAD95 CRC64;

Query Match 23.9%; Score 325.5; DB 2; Length 375;
 Best Local Similarity 30.5%; Pred. No. 4e-16;
 Matches 90; Conservative 40; Mismatches 72; Indels 93; Gaps 11;

QY 26 QQBDLPCCDSNTKFCYNNYNNFSSQPRHCKACRYWTHGTLRDVPPVCGGCRKAKR 85
 DB 70 KKKLNCPCRCSTVTKFCYNNYNNYSLQPRFYCKTCRRYWTGSLRNVPVGGSSRKRS 129
 QY 86 SRTCSNSSSSSSSVGSVNSNGVPL-----QTPVLP----- 117
 DB 130 SSSVVPBAASASISAVSSSVPLVGLAKNPKLHNEGADLNLAFRHNGRLQPRFETA 189
 QY 118 -----QSSISN--GVTHVTESDGKSAISLCSFTSTLLNHN----- 154
 DB 190 PPSLESSSVCPGNCGLAANAGCGRSV---GAFSAMELLRSTGYVPLQMAPLQMPA 245
 QY 155 --AATATN-----GSGSVIGIG-----GFGIGGSG--FDDVSFPL----- 186
 DB 246 EYLAAGFHLGFRMPPPPPQOOOQVTLGFLDTGAGAGGSGVFGACSAQLQSSAA 305
 QY 187 GRAMPFSTVGTATTNVG--SNGCHAVPMPATWQFEGLESNAGGFGVSGEYPA 239
 DB 306 GRLLFPFDLKPVSAAAGDANSGDH-----QYDHGNGCGGSGVIGGHEA 352

RESULT 15

Q6F2M0 PRELIMINARY; PRT; 371 AA.
 AC 06F2M0;
 DT 25-OCT-2004 (TReMBLrel. 28, Created)
 DT 25-OCT-2004 (TReMBLrel. 28, Last sequence update)
 DT 25-OCT-2004 (TReMBLrel. 28, Last annotation update)
 DE Putative Dof zinc finger protein.
 GN Name=OSJNBa010D2.15;
 OS Oryza sativa (japonica cultivar-group).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Erihartoideae; Oryzaceae; Oryza.
 OX NCBI_TaxID=39947;
 RN
 RP SEQUENCE FROM N.A.
 RA Buell C.R., Yuan Q., Ouyang S., Liu J., Ganeberger K., Jones K.M.,
 RA Overton I.T., Teltrin T., Kim M.M., Bera J.J., Jin S.S.,
 RA Fadrosh D.W., Tallon L.J., Koo H., Zismann V., Hsiao J., Blunt S.,
 RA Vanaken S.S., Riedmuller S.B., Utecherack T.V., Feldblum T.V.,
 RA Yang Q.O., Haas B.J., Suh B.B., Peterson J.J., Quackenbush J.,
 RA White O., Salzberg S.L., Fraser C.M.;
 RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
 RN
 RP SEQUENCE FROM N.A.

RA Buell R.;
 RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AC133003; AAT7633.1; -.
 DR GO; GO:0003677; F:DNA binding; IEA.
 DR InterPro; IPR002202; HMG-COA_red.
 DR InterPro; IPR003851; Znf_Dof.
 DR Pfam; PF02701; Zf-Dof; 1.
 DR PROSITE; PS00318; HMG_COA_REDUCTASE_2; UNKNOWN_1.
 DR PROSITE; PS01361; ZF_DOF_1; UNKNOWN_1.
 DR PROSITE; PSS0884; ZF_DOF_2; 1.
 SQ SEQUENCE 371 AA; 3681 MW; 2B409179ABCB0D798 CRC64;

Query Match 23.6%; Score 322; DB 2; Length 371;
 Best Local Similarity 35.2%; Pred. No. 7.3e-16;
 Matches 89; Conservative 24; Mismatches 76; Indels 64; Gaps 12;

QY 5 DSGEPRIAMKPNGVTV---PISDQEQLP-----CPRCDSSNTKFCYNNY 48
 DB 8 DAVVPRKGA-GGGGTTTPPPPPAQQOQOPLPPPPPEOGLRCPCDSNTKFCYNNY 66
 QY 49 NFSQPRHFCACRRYWTHGTLRDVPGGTRKSAKRSRTCSNSSSVGSVNSNGVPL 108
 DB 67 SLQPRHFCCTCRRYWTKGALNVPVGGGCRKN-KRSNAAAASRLSLN----- 115
 QY 109 LQTPVLPQSSISNGVTHVTESDGKSA--LSLCSFTSTLLNHN-----AATATN 160
 DB 116 LPTV-----EGIGAAADPAAAAAARLFLGGGTTMMSSSTSLGAAAAVADF 165
 QY 161 GSGSVIGI-----GFGIGGSGFDDVSGLGRAMPFSTVGTATTNVGSGNGH 211
 DB 166 QQGAAGVGMPLPRLQSPAGGAGV---HGYVPPG---EWPSSGDIAGNAVNGG--GGHG 216
 QY 212 AVPMPTWQFEG 224
 DB 217 AVSSTIASSTESL 229

Search completed: November 3, 2005, 16:13:23
 Job time : 62 secs

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OM protein - protein search, using SW model

Run on: November 3, 2005, 16:10:40 ; Search time 43 Seconds
(without alignment)
439.214 Million cell updates/sec

Title: US-10-509-691-2
Perfect score: 1163
Sequence: 1 MPTSDSGPRRIAKKPNQVT.....SGEYFAMPDLSTTPGSLK 253

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:
1: /cgn2_6/ptodata/1/1aa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/1aa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/1aa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/1aa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/1aa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/1aa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	298.5	21.9	214	4 US-09-598-401C-70	Sequence 70, Appl
2	253.5	18.6	60	4 US-09-434-840-6	Sequence 6, Appl
3	129	9.5	712	4 US-09-248-796A-14274	Sequence 14274, A
4	123	9.0	1160	3 US-08-808-599A-24	Sequence 24, Appl
5	119	8.7	674	1 US-08-317-522A-3	Sequence 3, Appl
6	119	8.7	674	1 US-08-439-818A-3	Sequence 3, Appl
7	119	8.7	674	2 US-08-751-965-3	Sequence 3, Appl
8	119	8.7	674	2 US-08-738-975-3	Sequence 3, Appl
9	119	8.7	674	2 US-08-728-626-3	Sequence 3, Appl
10	119	8.7	674	3 US-08-808-599A-3	Sequence 3, Appl
11	113	8.3	749	1 US-08-317-522A-2	Sequence 2, Appl
12	113	8.3	749	1 US-08-439-818A-2	Sequence 2, Appl
13	113	8.3	749	2 US-08-751-965-2	Sequence 2, Appl
14	113	8.3	749	2 US-08-738-975-2	Sequence 2, Appl
15	113	8.3	749	2 US-08-728-626-2	Sequence 2, Appl
16	113	8.3	749	3 US-08-808-599A-2	Sequence 2, Appl
17	108.5	8.0	749	4 US-09-248-796A-17283	Sequence 17283, A
18	103.5	7.6	553	4 US-09-242-913B-13	Sequence 13, Appl
19	103	7.5	975	4 US-09-328-352-4764	Sequence 4764, Ap
20	102.5	7.5	449	2 US-08-927-394-2	Sequence 2, Appl
21	102.5	7.5	449	4 US-09-538-092-1372	Sequence 1372, Ap
22	102.5	7.5	449	4 US-09-949-016-6604	Sequence 6604, Ap
23	102.5	7.5	563	4 US-09-949-016-10153	Sequence 10153, A
24	102	7.5	231	4 US-09-248-796A-14281	Sequence 14281, A
25	102	7.5	353	2 US-08-687-702-37	Sequence 37, Appl
26	102	7.5	618	4 US-09-248-796A-19273	Sequence 19273, A
27	102	7.5	2090	4 US-09-538-092-1081	Sequence 1081, Ap

28	102	7.5	2120	4 US-09-949-016-9768	Sequence 9768, Ap
29	101.5	7.4	522	4 US-09-538-092-1096	Sequence 1096, Ap
30	100.5	7.4	195	4 US-09-252-991A-18814	Sequence 18814, A
31	98.5	7.2	2110	4 US-09-270-767-46547	Sequence 46547, A
32	98	7.2	258	4 US-09-248-796A-23723	Sequence 23723, A
33	97.5	7.2	970	4 US-09-270-767-42741	Sequence 42741, A
34	97	7.1	155	1 US-08-209-747-15	Sequence 15, Appl
35	97	7.1	155	1 US-08-458-298-15	Sequence 15, Appl
36	97	7.1	213	4 US-09-489-039A-11130	Sequence 11130, A
37	97	7.1	832	1 US-08-209-747-2	Sequence 2, Appl
38	97	7.1	832	1 US-08-458-298-2	Sequence 2, Appl
39	95.5	7.0	1227	1 US-08-448-170-8	Sequence 8, Appl
40	95.5	7.0	1227	3 US-08-961-803-9	Sequence 9, Appl
41	95.5	7.0	1227	4 US-09-661-332A-63	Sequence 63, Appl
42	95	7.0	1026	1 US-08-194-280-7	Sequence 7, Appl
43	95	7.0	1026	2 US-08-614-377A-7	Sequence 7, Appl
44	95	7.0	1026	4 US-09-142-648B-7	Sequence 7, Appl
45	94.5	6.9	222	4 US-09-545-216A-2	Sequence 2, Appl

ALIGNMENTS

```
RESULT 1
US-09-598-401C-70
; Sequence 70, Application US/09598401C
; Patent No. 6596925
; GENERAL INFORMATION:
; APPLICANT: Perera, J. Ranjan
; APPLICANT: Eagleton, Clare
; TITLE OF INVENTION: Compositions and Methods for the
; TITLE OF INVENTION: Modification of Gene Expression
; FILE REFERENCE: 11000.1036C2
; CURRENT FILING DATE: US/09/598, 401C
; PRIOR FILING DATE: 2000-06-20
; PRIOR APPLICATION NUMBER: U.S. No. 6596925 60/146,591
; PRIOR FILING DATE: 1999-07-30
; PRIOR APPLICATION NUMBER: PCT/NZ00/00018
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: U.S. No. 6596925 09/276,599
; PRIOR FILING DATE: 1999-03-25
; NUMBER OF SEQ ID NOS: 120
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 70
; LENGTH: 214
; TYPE: PRT
; ORGANISM: Eucalyptus grandis
US-09-598-401C-70

Query Match      21.9% Score 298.5; DB 4; Length 214;
Best Local Similarity 46.0%; Pred. No. 7.4e-20;
Matches 69; Conservative 16; Mismatches 48; Indels 17; Gaps 6;

QY 23 ISDOOEQ-LPQPCDSSNTKFCYNNYVFSQPRHFKCAKRRYWTHTGTLRDVPVGGGTRK 81
DB 14 IKPQTEQLKPKPRCDSTYTKFCYNNYVLSQPRHFKCKRYWTGGLRVVPGGGGRK 73
QY 82 SAKSRRTCSN--SSSSSVGVVNSNGVPLQTPVLPQS--SISNGVHTVTTESDGKSA 138
DB 74 NKRAKRAVDHVSQKNEASTSAAPGNEVP--DRSPFEPSSKSIYYG-----GEN 121
QY 139 LSLGSGFTSTLLNNAATATHGSGSVIGI 168
DB 122 MWLTG-LPFSRIQDRALAHCHNSSSFLGM 150

RESULT 2
US-09-434-840-6
; Sequence 6, Application US/09434840
; Patent No. 6620985
; GENERAL INFORMATION:
; APPLICANT: Glazebrook, Jane
```

```

: APPLICANT: Jirage, Dayadevi
: APPLICANT: Toocle, Tina L
: APPLICANT: Zhou, Nan
: APPLICANT: Feys, Bart
: TITLE OF INVENTION: PAD4 COMPOSITIONS AND METHODS THEREFOR
: FILE REFERENCE: 043503.0009
: CURRENT APPLICATION NUMBER: US/09/434,840
: CURRENT FILING DATE: 1999-11-04
: EARLIER APPLICATION NUMBER: 09/190,733
: EARLIER FILING DATE: 1998-11-12
: NUMBER OF SEQ ID NOS: 85
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO: 6
: LENGTH: 60
: TYPE: PRT
: ORGANISM: Arabidopsis thaliana
US-09-434-840-6

```

```

Query Match 18.6%; Score 253.5; DB 4; Length 60;
Best Local Similarity 72.9%; Pred. No. 2e-16;
Matches 43; Conservative 8; Mismatches 7; Indels 1; Gaps 1;

```

```

QY 32 CPCRDSSTKCYNNNNYFSGPRHCKRCRYWTHGTLRPVGGGRKAKSRCTCS 90
DB 2 CPCRDSSTKCYNNNNYSLTQPRYFCGCRRYWTKGSLRNVPGGGRKSS 59

```

```

RESULT 3
US-09-248-796A-14274
: Sequence 14274, Application US/09248796A
: Patent No. 6747137
: GENERAL INFORMATION:
: APPLICANT: Keith Weinstock et al
: TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
: TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
: FILE REFERENCE: 107196.132
: CURRENT APPLICATION NUMBER: US/09/248,796A
: CURRENT FILING DATE: 1999-02-12
: PRIOR APPLICATION NUMBER: US 60/074,725
: PRIOR FILING DATE: 1998-02-13
: PRIOR APPLICATION NUMBER: US 60/096,409
: PRIOR FILING DATE: 1998-08-13
: NUMBER OF SEQ ID NOS: 28208
: SEQ ID NO 14274
: LENGTH: 712
: TYPE: PRT
: ORGANISM: Candida albicans
US-09-248-796A-14274

```

```

Query Match 9.5%; Score 129; DB 4; Length 712;
Best Local Similarity 26.0%; Pred. No. 0.002;
Matches 58; Conservative 27; Mismatches 60; Indels 78; Gaps 12;

```

```

QY 89 CSNSSSSSVSGV-----VSNSNGVPLQTTPLFPQSSISNGVHTTTHESDGK 136
DB 459 CFESTTLVSSVPCPTQVPGVFTSTDNHGVPIASIDVTGAATVSN---TIKAODSTG 514
QY 137 -----SALSLGSGFTSTLNLH-----NAAATATHSGSVYIGGFGIGLGSFDD 181
DB 515 FTSAGNATITATITATGATTTVSGGSGSTIDYNAAGTTIAAGSGDSG--SGSGSGSGSSSS 573
QY 182 VSFGI-----GRAMPFSTVGTAT-----TTNVGSN-----GG 209
DB 574 NTVGIVNPKVSSAASGITVAASASAGS--WPYSSGSGGNGVPLGANNVGSGTPTVSG 632
QY 210 HHAVPMATWQFEGLESNAGCGFVSGEYFAMPDLSTTPGSL 252
DB 633 GNSNPSTVTGAAGV-----GGVSGS-----PSYS-----GNSL 662

```

```

RESULT 4
US-08-808-599A-24
: Sequence 24, Application US/0808599A

```

```

: Patent No. 611089
: GENERAL INFORMATION:
: APPLICANT: Fukuda, Michiko N.
: TITLE OF INVENTION: Trophinin, Trophinin-Assisting
: TITLE OF INVENTION: Proteins and Methods to Inhibit Implantation
: NUMBER OF SEQUENCES: 41
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Campbell & Flores LLP
: STREET: 4370 La Jolla Village Drive, Suite 700
: CITY: San Diego
: STATE: California
: COUNTRY: USA
: ZIP: 92122
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/808,599A
: FILING DATE: 28-FEB-1997
: CLASSIFICATION: 424
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/317,522
: FILING DATE: 04-OCT-1994
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/439,818
: FILING DATE: 12-MAY-1995
: ATTORNEY/AGENT INFORMATION:
: NAME: Campbell, Kathryn A.
: REGISTRATION NUMBER: 31,815
: REFERENCE/DOCKET NUMBER: P-LA 2256
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (619) 535-9001
: TELEFAX: (619) 535-8949
: INFORMATION FOR SEQ ID NO: 24:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 1160 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: protein
US-08-808-599A-24

```

```

Query Match 9.0%; Score 123; DB 3; Length 1160;
Best Local Similarity 27.6%; Pred. No. 0.014;
Matches 64; Conservative 24; Mismatches 76; Indels 68; Gaps 14;

```

```

QY 67 GGTLRD-VPIVGGTRKSARKSRCTCSN-----SSSSSVSGVVSNSN----- 105
DB 681 GGALNNNSAGFGAISTSPGALNNNSAGFGAISTVASFGAISNPDGAFSTSVGF 740
QY 106 GVPLOTT-----PVLFF-----POSSISNGVHTTTHESDGKSLSLC-GSFTSTLL--- 150
DB 741 GGTLLNTDPSGNSHNSISFSGAPTTTSVSGSHSTNLCFGGAISTSLCFPSASNTNLCPG 800
QY 151 -----NHNAATATHSGSVIGI-----GFGIGLG--SGFDD---VSFGIGRAMWP 192
DB 801 GSNSTNCFSGATSANFEGHISIFGNGLSISAGFGNGLGTISAGFDDSLGTSTGFGSLGP 860
QY 193 FSTVGTATTTNVNSNGHNAVMPATWQF--GLEUNA--GG-----GPIVSG 235
DB 861 SASFNGLGTSTGFGG-----LGTSTDFGGINHADFNFGIGNSAGFNGG 907

```

```

RESULT 5
US-08-317-522A-3
: Sequence 3, Application US/08317522A
: Patent No. 5599918
: GENERAL INFORMATION:
: APPLICANT: Fukuda, Michiko N.
: TITLE OF INVENTION: Trophinin and Trophinin-Assisting
: TITLE OF INVENTION: Proteins
: NUMBER OF SEQUENCES: 13

```


CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/439,818
FILING DATE: 12-MAY-1995
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-LA 2252
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 674 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-751-965-3

Query Match 8.7%; Score 119; DB 2; Length 674;
Best Local Similarity 24.9%; Pred. No. 0.016;
Matches 65; Conservative 18; Mismatches 76; Indels 102; Gaps 11;

QY 67 GGT-ROVPVGGGRKSA-----KSRITCSNSSSSSVGVVNS---NGVPLQTPV 114
DB 290 GGTLSVVCFGSPSTSAFGGALNTNASFGCAVSTSAFSGAVSTSAFSGAPI-TNPG 348
QY 115 L-----FPQSSISNGVTHVTESDGKSAALSLC-GSFTSTLLN 151
DB 349 FGCAFTSAGFGALSTADFGCTPSNIGFGAAPSTSVSFGAHGTSLCFGGAPSTSLC 408
QY 152 HNAATA-----THGSGSVIGI-----GFG 172
DB 409 FGSAINTNLCPFPPSTSAFSGATSPSPCDGPSTSTGTFGNGLSTGFGGLNTSAGFG 468
QY 173 IGLG-----SGFD---DVSRGLGRAMPSTVGTATTNTVNGSGHHAVMPA 217
DB 469 GGLTSAFSGGSLTSSGFDGLGTSAGFGGPGTSTGFGGGLTSAFSGG-----520
QY 218 TWOFEGLSNAGGFGVSGEYF 238
DB 521 ----LGTSAFGGGLVTSDFG 537

RESULT 8
US-08-738-975-3
Sequence 3, Application US/08738975
Patent No. 5880267
GENERAL INFORMATION:
APPLICANT: Fukuda, Michiko N.
TITLE OF INVENTION: Trophinin and Trophinin-Assisting
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell and Flores
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: USA
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/738,975
FILING DATE: herewith
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/439,818
FILING DATE: 05-Dec-1995
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.

REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-LA 2251
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 674 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-738-975-3

Query Match 8.7%; Score 119; DB 2; Length 674;
Best Local Similarity 24.9%; Pred. No. 0.016;
Matches 65; Conservative 18; Mismatches 76; Indels 102; Gaps 11;

QY 67 GGT-ROVPVGGGRKSA-----KSRITCSNSSSSSVGVVNS---NGVPLQTPV 114
DB 290 GGTLSVVCFGSPSTSAFGGALNTNASFGCAVSTSAFSGAVSTSAFSGAPI-TNPG 348
QY 115 L-----FPQSSISNGVTHVTESDGKSAALSLC-GSFTSTLLN 151
DB 349 FGCAFTSAGFGALSTADFGCTPSNIGFGAAPSTSVSFGAHGTSLCFGGAPSTSLC 408
QY 152 HNAATA-----THGSGSVIGI-----GFG 172
DB 409 FGSAINTNLCPFPPSTSAFSGATSPSPCDGPSTSTGTFGNGLSTGFGGLNTSAGFG 468
QY 173 IGLG-----SGFD---DVSRGLGRAMPSTVGTATTNTVNGSGHHAVMPA 217
DB 469 GGLTSAFSGGSLTSSGFDGLGTSAGFGGPGTSTGFGGGLTSAFSGG-----520
QY 218 TWOFEGLSNAGGFGVSGEYF 238
DB 521 ----LGTSAFGGGLVTSDFG 537

RESULT 9
US-08-728-626-3
Sequence 3, Application US/08728626
Patent No. 5910451
GENERAL INFORMATION:
APPLICANT: Fukuda, Michiko N.
TITLE OF INVENTION: Trophinin and Trophinin-Assisting
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell and Flores
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: USA
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/728,626
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/439,818
FILING DATE: 12-MAY-1995
APPLICATION NUMBER: US 08/317,522
FILING DATE: 04-OCT-1994
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-LA 1563
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001

TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 674 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-728-626-3

Query Match 8.7%; Score 119; DB 2; Length 674;
Best Local Similarity 24.9%; Pred. No. 0.016;

Matches 65; Conservative 18; Mismatches 76; Indels 102; Gaps 11;

QY 67 GGTLDVPGVGGTRKSA-----KSRRTCSNSSSSVSGVNS---NGVPLQTTPV 114
DB 290 GGTLDVPGVGGTRKSA-----KSRRTCSNSSSSVSGVNS---NGVPLQTTPV 114
QY 115 L-----PPOSSISNGVTHVTESDGKSGALSLC-GSFTSTLLN 151
DB 349 FGAFSTAGFGALSTADFGCTPSNIGFGAAPSTSVSFGAGHSTLCFGAPSTSLC 408
QY 152 HNAATA-----THGSGSVIGI-----GFG 172
DB 409 FGASANTNLFCGPPSTACFSGATSPFCDDPSTSTGSPFGNGLSTGFGGLNTSAGFG 468
QY 173 IGLG-----SGFD---DVSFGLGRAMPFSTVGTATTNNVSGNGHVAVMPA 217
DB 469 GGLGTSAGFSGGLSTSSGFDGLGTSAGFGGPGTSTGFGGLGTSAGFSGG----- 520
QY 218 TWOFEGLSNAGGFGVSGEYF 238
DB 521 ----LGTSAFGGGLVTSDF 537

RESULT 10
US-08-808-599A-3

Sequence 3, Application US/08808599A

Patent No. 6111089

GENERAL INFORMATION:

APPLICANT: Fukuda, Michiko N.

TITLE OF INVENTION: Trophinin, Trophinin-Assisting

TITLE OF INVENTION: Proteins and Methods to Inhibit Implantation

NUMBER OF SEQUENCES: 41

CORRESPONDENCE ADDRESS:

ADDRESSEE: Campbell & Flores LLP

STREET: 4370 La Jolla Village Drive, Suite 700

CITY: San Diego

STATE: California

COUNTRY: USA

ZIP: 92122

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/808,599A

FILING DATE: 28-FEB-1997

CLASSIFICATION: 424

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/317,522

FILING DATE: 04-OCT-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/439,818

FILING DATE: 12-MAY-1995

ATTORNEY/AGENT INFORMATION:

NAME: Campbell, Cathryn A.

REGISTRATION NUMBER: 31,815

REFERENCE/DOCKET NUMBER: P-LA 2256

TELECOMMUNICATION INFORMATION:

TELEPHONE: (619) 535-9001

TELEFAX: (619) 535-8949

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 674 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-808-599A-3

Query Match 8.7%; Score 119; DB 3; Length 674;
Best Local Similarity 24.9%; Pred. No. 0.016;

Matches 65; Conservative 18; Mismatches 76; Indels 102; Gaps 11;

QY 67 GGTLDVPGVGGTRKSA-----KSRRTCSNSSSSVSGVNS---NGVPLQTTPV 114
DB 290 GGTLDVPGVGGTRKSA-----KSRRTCSNSSSSVSGVNS---NGVPLQTTPV 114
QY 115 L-----PPOSSISNGVTHVTESDGKSGALSLC-GSFTSTLLN 151
DB 349 FGAFSTAGFGALSTADFGCTPSNIGFGAAPSTSVSFGAGHSTLCFGAPSTSLC 408
QY 152 HNAATA-----THGSGSVIGI-----GFG 172
DB 409 FGASANTNLFCGPPSTACFSGATSPFCDDPSTSTGSPFGNGLSTGFGGLNTSAGFG 468
QY 173 IGLG-----SGFD---DVSFGLGRAMPFSTVGTATTNNVSGNGHVAVMPA 217
DB 469 GGLGTSAGFSGGLSTSSGFDGLGTSAGFGGPGTSTGFGGLGTSAGFSGG----- 520
QY 218 TWOFEGLSNAGGFGVSGEYF 238
DB 521 ----LGTSAFGGGLVTSDF 537

RESULT 11
US-08-317-522A-2

Sequence 2, Application US/08317522A

Patent No. 559918

GENERAL INFORMATION:

APPLICANT: Fukuda, Michiko N.

TITLE OF INVENTION: Trophinin and Trophinin-Assisting

TITLE OF INVENTION: Proteins

NUMBER OF SEQUENCES: 13

CORRESPONDENCE ADDRESS:

ADDRESSEE: Campbell and Flores

STREET: 4370 La Jolla Village Drive, Suite 700

CITY: San Diego

STATE: California

COUNTRY: USA

ZIP: 92122

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/317,522A

FILING DATE: 04-OCT-1994

CLASSIFICATION: 536

ATTORNEY/AGENT INFORMATION:

NAME: Campbell, Cathryn A.

REGISTRATION NUMBER: 31,815

REFERENCE/DOCKET NUMBER: P-LA 9991

TELECOMMUNICATION INFORMATION:

TELEPHONE: (619) 535-9001

TELEFAX: (619) 535-8949

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 749 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-317-522A-2

Query Match 8.3%; Score 113; DB 1; Length 749;
Best Local Similarity 25.1%; Pred. No. 0.066;

Matches 66; Conservative 19; Mismatches 74; Indels 104; Gaps 12;

[illegible]

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1      RESULT 12
2      US-08-439-818A-2
3      ; Sequence 2, Application US/08439818A
4      Patent No. 5654145
5      GENERAL INFORMATION:
6      APPLICANT: Fukuda, Michiko N.
7      TITLE OF INVENTION: Trophinin and Trophinin-Assisting
8      TITLE OF INVENTION: Proteins
9      NUMBER OF SEQUENCES: 22
10     CORRESPONDENCE ADDRESS:
11     ADDRESSEE: Campbell and Flores
12     STREET: 4370 La Jolla Village Drive, Suite 700
13     CITY: San Diego
14     STATE: California
15     COUNTRY: USA
16     ZIP: 92122
17     COMPUTER READABLE FORM:
18     MEDIUM TYPE: Floppy disk
19     COMPUTER: IBM PC compatible
20     OPERATING SYSTEM: PC-DOS/MS-DOS
21     SOFTWARE: PatentIn Release #1.0, Version #1.25
22     CURRENT APPLICATION DATA:
23     APPLICATION NUMBER: US/08/439,818A
24     FILING DATE: 12-May-1995
25     CLASSIFICATION: 435
26     PRIOR APPLICATION DATA:
27     APPLICATION NUMBER: US 08/317,522
28     FILING DATE: 04-OCT-1994
29     ATTORNEY/AGENT INFORMATION:
30     NAME: Campbell, Cathryn A.
31     REGISTRATION NUMBER: 31,815
32     TELECOMMUNICATION INFORMATION:
33     REFERENCE/DOCKET NUMBER: P-LA 1563
34     TELEPHONE: (619) 535-9001
35     TELEFAX: (619) 535-8949
36     INFORMATION FOR SEQ ID NO: 2:
37     SEQUENCE CHARACTERISTICS:
38     LENGTH: 749 amino acids
39     TYPE: amino acid
40     TOPOLOGY: linear
41     MOLECULE TYPE: protein
42     US-08-439-818A-2

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Query Match	8.3%	Score	113	DB	1	Length	749
Best Local Similarity	25.1%	Pred.	No.	0.066			
Matches	66	Conservative	19	Mismatches	74	Indels	104
				Gaps			12

Dy 67 GGTL-RDVPVGGGTRKSA-----KRSRCTSSSSSSSVSGVSN---NGVPLQTTTPV 114
||| : : : : :
Db 358 GGTLTSTVCFCGSPSTRSAGFGALNTNVAFCGAVSTASFCGAVSTACFSGAPI -TNPg 416

```

QY      115  L-----PQSSISNVNTHVTESDQKSLSLIC-GEFTSTLNLN 151
           : : : : : : : : : : : : : : : : : : : :
Db      417  FCGAFTSAGFCGALSTADFCGCTSNISIGFGAAFTSVISFCGAHGTSLICFGAPSTSLC 476
           : : : : : : : : : : : : : : : : : : : :
QY      152  HNA-----ATA-----HGSGSVTIG-----G 170
           : : : : : : : : : : : : : : : : : : : :
Db      477  FGSAENTNLCFCGPSTACFCGATSPSPCDGPSTSTGSPFGGLSTNAGFCGGLNTSAG 536
           : : : : : : : : : : : : : : : : : : : :
QY      171  FGIIG-----SGPD---DVSPGLGRAMPSTVGTATTNNGNGCHNAVPM 215
           : : : : : : : : : : : : : : : : : : : :
Db      537  FCGGIGTSAGFSGGLSTSSGFGGLCTSGAGGCGPRTSGFGGGLCTSGAGFSG----- 590
           : : : : : : : : : : : : : : : : : : : :
QY      216  PATWQFEGLESNAGGAFVSGEYF 238
           : : : : : : : : : : : : : : : : : : : :
Db      591  -----LGTSAFGGGLVTSDFG 607
           : : : : : : : : : : : : : : : : : : : :

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1      RESULT 13
2      US-08-751-965-2
3      / Sequence 2, Application US/08751965
4      / Patent No. 568360
5      / GENERAL INFORMATION:
6      / APPLICANT: Fukuda, Michiko N.
7      / TITLE OF INVENTION: Trophinin and Trophinin-Assisting
8      / TITLE OF INVENTION: Proteins
9      / NUMBER OF SEQUENCES: 22
10     / CORRESPONDENCE ADDRESS:
11     / ADDRESSEE: Campbell and Flores
12     / STREET: 4370 La Jolla Village Drive, Suite 700
13     / CITY: San Diego
14     / STATE: California
15     / COUNTRY: USA
16     / ZIP: 92122
17     / COMPUTER READABLE FORM:
18     / MEDIUM TYPE: Floppy disk
19     / COMPUTER: IBM PC compatible
20     / OPERATING SYSTEM: PC-DOS/MS-DOS
21     / SOFTWARE: patentin Release #1.0, Version #1.25
22     / CURRENT APPLICATION DATA:
23     / APPLICATION NUMBER: US/08/751,965
24     / FILING DATE: Herewith
25     / CLASSIFICATION:
26     / PRIOR APPLICATION DATA:
27     / APPLICATION NUMBER: US 08/439,818
28     / FILING DATE: 12-MAY-1995
29     / ATTORNEY/AGENT INFORMATION:
30     / NAME: Campbell, Cathryn A.
31     / REGISTRATION NUMBER: 31,815
32     / REFERENCE/DOCKET NUMBER: P-LA 2252
33     / TELECOMMUNICATION INFORMATION:
34     / TELEPHONE: (619) 535-9001
35     / TELEFAX: (619) 535-8949
36     / INFORMATION FOR SEQ ID NO: 2:
37     / SEQUENCE CHARACTERISTICS:
38     / LENGTH: 749 amino acids
39     / TYPE: amino acid
40     / TOPOLOGY: linear
41     / MOLECULE TYPE: protein
42     / US-08-751-965-2

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Query Match	8.3%	Score 113;	DB 2;	Length 749
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QY 171 FGIGIG-----SGPD---DVSFGLGRAMMPSTVTGATTNNVSGNGHHAVPM 215
Db 537 FGGGLTSAAGSGGLSTSSGFDGLTSAAGFGGPGTSTGFGGGLTSAAGFCG----- 590
QY 216 PATWQFGLBESNAGGFPVSGEYF 238
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RESULT 14
US-08-738-975-2
; Sequence 2, Application US/08738975
; Patent No. 5880267

; GENERAL INFORMATION:
; APPLICANT: Fukuda, Michiko N.
; TITLE OF INVENTION: Trophinin and Trophinin-Aesistering
; TITLE OF INVENTION: Proteins
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell and Flores
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/738,975
; FILING DATE: herewith
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/439,818
; FILING DATE: 05-Dec-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-LA 2251
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 749 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-738-975-2

Query Match 8.3%; Score 113; DB 2; Length 749;
Best Local Similarity 25.1%; Pred. No. 0.066; Indels 104; Gaps 12;
Matches 66; Conservative 19; Mismatches 74;

QY 67 GGTI-RDVPVGGGTRKSA-----KSRRTCSNSSSSVSGVSN---NGVPLQTTTPV 114
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Db 591 -----LGTSAGFGGGLVTSDF 607

RESULT 15
US-08-728-626-2
; Sequence 2, Application US/08728626
; Patent No. 5910451

; GENERAL INFORMATION:
; APPLICANT: Fukuda, Michiko N.
; TITLE OF INVENTION: Trophinin and Trophinin-Aesistering
; TITLE OF INVENTION: Proteins
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell and Flores
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/728,626
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/439,818
; FILING DATE: 12-MAY-1995
; APPLICATION NUMBER: US 08/317,522
; FILING DATE: 04-OCT-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 749 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-728-626-2

Query Match 8.3%; Score 113; DB 2; Length 749;
Best Local Similarity 25.1%; Pred. No. 0.066;
Matches 66; Conservative 19; Mismatches 74; Indels 104; Gaps 12;

QY 67 GGTI-RDVPVGGGTRKSA-----KSRRTCSNSSSSVSGVSN---NGVPLQTTTPV 114
Db 358 GGTISTVCFGSPSTSAFCGALNTNASFCAVSTSAFSGAVSTSAFCGAPL-TNPG 416
QY 115 L-----PSSISNGVTHTVESDGKSLALIC-GSFTSTLNL 151
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QY 152 HNAA-----ATAT-----HSGSVYIGIG-----G 170
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Db 591 -----| : ||| | : |
-----LGTSAFGGGLVTSDDF 607

Search completed: November 3, 2005, 16:14:33
Job time : 45 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 3, 2005, 16:11:06 ; Search time 167 Seconds
(without alignments)
633.878 Million cell updates/sec

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Perfect score: 133
Sequence: 1 MPTSDGEPRIAMKNGVT.....SGEYFAPDLSITPGNSLK 253

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867879 seqs, 418409474 residues

Total number of hits satisfying chosen parameters: 1867879

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	651	47.8	225	US-10-225-066A-128	Sequence 128, App
2	651	47.8	225	US-10-225-067-6	Sequence 6, App1
3	651	47.8	225	US-10-374-780A-2760	Sequence 2760, App
4	651	47.8	225	US-10-225-066A-128	Sequence 128, App
5	436.5	33.0	156	US-10-424-599-268677	Sequence 268677, App
6	402	29.5	209	US-10-225-066A-404	Sequence 404, App
7	402	29.5	209	US-10-374-780A-2762	Sequence 2762, App
8	402	29.5	209	US-10-225-066A-404	Sequence 404, App
9	377.5	27.7	204	US-10-225-066A-406	Sequence 406, App
10	377.5	27.7	204	US-10-374-780A-362	Sequence 362, App
11	377.5	27.7	204	US-10-225-066A-406	Sequence 406, App

12	377.5	27.7	206	US-10-425-114-40748	Sequence 40748, A
13	376.5	27.6	211	US-10-424-599-187121	Sequence 187121, A
14	376.5	27.6	211	US-10-425-114-43084	Sequence 43084, A
15	356	26.1	211	US-10-424-599-239234	Sequence 239234, A
16	355	26.0	211	US-10-424-599-239232	Sequence 239232, A
17	352	25.8	383	US-10-425-115-205283	Sequence 205283, A
18	341	25.0	401	US-10-425-114-46978	Sequence 46978, A
19	335	24.6	300	US-10-424-599-219343	Sequence 219343, A
20	335	24.6	324	US-10-424-599-218016	Sequence 218016, A
21	335	24.6	329	US-10-425-114-37734	Sequence 37734, A
22	335	24.6	352	US-10-425-114-56897	Sequence 56897, A
23	334	24.5	220	US-10-437-963-193177	Sequence 193177, A
24	333.5	24.5	339	US-10-425-114-42241	Sequence 42241, A
25	333.5	24.5	339	US-10-425-114-53358	Sequence 53358, A
26	333.5	24.5	341	US-10-424-599-200270	Sequence 200270, A
27	331	24.3	378	US-10-425-114-57083	Sequence 57083, A
28	331	24.3	378	US-10-425-115-199078	Sequence 199078, A
29	330.5	24.2	244	US-10-425-115-298984	Sequence 298984, A
30	330.5	24.2	275	US-10-425-114-53945	Sequence 63945, A
31	328	24.1	389	US-10-437-963-162230	Sequence 162230, A
32	328	24.1	452	US-10-437-963-162233	Sequence 162233, A
33	327	24.0	328	US-10-425-115-259592	Sequence 259592, A
34	327	24.0	330	US-10-425-114-37762	Sequence 37762, A
35	326	23.9	329	US-10-425-114-38607	Sequence 38607, A
36	326	23.9	348	US-10-424-599-199578	Sequence 199578, A
37	325.5	23.9	375	US-10-437-963-117427	Sequence 117427, A
38	325	23.8	333	US-10-425-114-57014	Sequence 57014, A
39	325	23.8	352	US-10-425-115-191735	Sequence 191735, A
40	325	23.8	347	US-10-425-115-204367	Sequence 204367, A
41	323	23.7	348	US-10-437-963-124974	Sequence 124974, A
42	323	23.7	366	US-10-425-115-342526	Sequence 342526, A
43	322.5	23.7	360	US-10-739-930-13883	Sequence 7383, App
44	322	23.6	371	US-10-437-963-124876	Sequence 124876, A
45	321.5	23.6	355	US-10-437-963-191965	Sequence 191965, A

ALIGNMENTS

RESULT 1
US-10-225-066A-128
; Sequence 128, Application US/10225066A
; Publication No. US20030226173A1
GENERAL INFORMATION:
; APPLICANT: Mendel Biotechnology, Inc.
; APPLICANT: RATCLIFFE, Oliver
; APPLICANT: RIECHMANN, Jose Luis
; APPLICANT: ADAM, Luc J
; APPLICANT: DUBELL, Arnold T
; APPLICANT: HEARD, Jacqueline E
; APPLICANT: JIANG, Cai-Zhong
; APPLICANT: REUBER, T. Lynne
; APPLICANT: CREELMAN, Robert A
; APPLICANT: PINEDA, Omeira
; APPLICANT: YU, Guo-Liang
; APPLICANT: BROWN, Pierre E
; TITLE OF INVENTION: Yield-Related Polynucleotides and Polypeptides in Plants
; FILE REFERENCE: ME10036-2 US
; CURRENT APPLICATION NUMBER: US/10/225, 066A
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: 09/837,444
; PRIOR FILING DATE: 2001-04-18
; PRIOR APPLICATION NUMBER: 60/310,847
; PRIOR FILING DATE: 2001-08-09
; PRIOR APPLICATION NUMBER: 60/336,049
; PRIOR FILING DATE: 2001-12-05
; PRIOR APPLICATION NUMBER: 60/338,692
; PRIOR FILING DATE: 2001-12-11
; PRIOR APPLICATION NUMBER: 10/171,468
; PRIOR FILING DATE: 2002-06-14
; NUMBER OF SEQ ID NOS: 1122
; SOFTWARE: PatentIn version 3.1

SEQ ID NO 128
LENGTH: 225
TYPE: PRT
ORGANISM: Arabidopsis thaliana
US-10-225-066A-128

Query Match 47.8%; Score 651; DB 15; Length 225;
Best Local Similarity 55.5%; Pred. No. 8.5e-52;
Matches 137; Conservative 31; Mismatches 49; Indels 30; Gaps 10;

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QY 117 POSSISNGVTHVTYESDGKSAISLCSFTSTLNNHNAATATHGSGSVIGIGFGIGLG 176
DB 115 POSSSNGGIT-----TAKGSASFGYGF-SSLINYNAAVSRNGPGGFGNPGDAFGLGLG 167
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DB 168 HGSYYEDVRYGQGITVWPFSSGATDAATTS-----HIAQIPATWQFEGQESKV--GF 218
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DB 219 VSGDYVA 225

RESULT 2

US-10-225-067-6
Sequence 6, Application US/10225067
Publication No. US20040019925A1
GENERAL INFORMATION:
APPLICANT: Mendel Biotechnology, Inc.
APPLICANT: Heard, Jacqueline E.
APPLICANT: Riechmann, Jose Luis
APPLICANT: Creelman, Robert A.
APPLICANT: Keddie, James
APPLICANT: Pilgrim, Martha L.
APPLICANT: Dubell, Arnold T.
APPLICANT: Jiang, Cai-Zhong
APPLICANT: Ratcliffe, Oliver
APPLICANT: Pineda, Omalra
APPLICANT: Yu, Guo-Liang
APPLICANT: Broun, Pierre E.
TITLE OF INVENTION: BIOCHEMISTRY-RELATED POLYNUCLEOTIDES AND
FILE REFERENCE: 51442002042
CURRENT APPLICATION NUMBER: US/10/225,067
PRIOR FILING DATE: 2002-08-09
PRIOR APPLICATION NUMBER: 60/310,847
PRIOR FILING DATE: 2001-08-09
PRIOR APPLICATION NUMBER: 60/336,049
PRIOR FILING DATE: 2001-11-19
PRIOR APPLICATION NUMBER: 60/338,692
PRIOR FILING DATE: 2001-12-11
PRIOR APPLICATION NUMBER: 10/171,468
PRIOR FILING DATE: 2002-06-14
NUMBER OF SEQ ID NOS: 148
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 6
LENGTH: 225
TYPE: PRT
ORGANISM: Arabidopsis thaliana
FEATURE:
NAME/KEY: DOMAIN
LOCATION: (34)...(62)
OTHER INFORMATION: Conserved domain
US-10-225-067-6

Query Match 47.8%; Score 651; DB 15; Length 225;
Best Local Similarity 55.5%; Pred. No. 8.5e-52;
Matches 137; Conservative 31; Mismatches 49; Indels 30; Gaps 10;

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RESULT 3

US-10-374-780A-2760
Sequence 2760, Application US/10374780A
Publication No. US20040019927A1
GENERAL INFORMATION:
APPLICANT: Sherman, Bradley K.
APPLICANT: Riechmann, Jose Luis
APPLICANT: Jiang, Cai-Zhong
APPLICANT: Heard, Jacqueline E.
APPLICANT: Haake, Volker
APPLICANT: Creelman, Robert A.
APPLICANT: Ratcliffe, Oliver
APPLICANT: Reuber, T. Lynne
APPLICANT: Adam, Luc J.
APPLICANT: Broun, Pierre E.
APPLICANT: Pilgrim, Martha L.
APPLICANT: Dubell III, Arnold T.
APPLICANT: Pineda, Omalra
APPLICANT: Yu, Guo-Liang
TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES IN PLANTS
FILE REFERENCE: MBI-0047 CIP
CURRENT APPLICATION NUMBER: US/10/374,780A
PRIOR FILING DATE: 2003-02-25
PRIOR APPLICATION NUMBER: 09/837,944
PRIOR FILING DATE: 2001-04-18
PRIOR APPLICATION NUMBER: 60/310,847
PRIOR FILING DATE: 2001-08-09
PRIOR APPLICATION NUMBER: 09/934,455
PRIOR FILING DATE: 2001-08-22
PRIOR APPLICATION NUMBER: 60/336,049
PRIOR FILING DATE: 2001-11-19
PRIOR APPLICATION NUMBER: 60/338,692
PRIOR FILING DATE: 2001-12-11
PRIOR APPLICATION NUMBER: 10/171,468
PRIOR FILING DATE: 2002-06-14
PRIOR APPLICATION NUMBER: 10/225,066
PRIOR FILING DATE: 2002-08-09
PRIOR APPLICATION NUMBER: 10/225,067
PRIOR FILING DATE: 2002-08-09
PRIOR APPLICATION NUMBER: 10/225,068
PRIOR FILING DATE: 2002-08-09
NUMBER OF SEQ ID NOS: 2906
SOFTWARE: PatentIn Version 3.2
SEQ ID NO 2760
LENGTH: 225
TYPE: PRT
ORGANISM: Arabidopsis thaliana

FEATURE:
OTHER INFORMATION: G1897
US-10-374-780A-2760

Query Match 47.8%; Score 651; DB 15; Length 225;
Best Local Similarity 55.5%; Pred. No. 8.5e-52;
Matches 137; Conservative 31; Mismatches 49; Indels 30; Gaps 10;

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RESULT 4

US-10-225-066A-128
Sequence 128, Application US/10225066A
Publication No. US20050160493A9
GENERAL INFORMATION:
APPLICANT: Mendel Biotechnology, Inc.
APPLICANT: RATCLIFFE, Oliver
APPLICANT: RIECHMANN, Jose Luis
APPLICANT: ADAM, Luc J
APPLICANT: DUBBEL, Arnold T
APPLICANT: HEARD, Jacqueline E
APPLICANT: PILGRIM, Maretha L
APPLICANT: JIANG, Cai-Zhong
APPLICANT: REUBER, T. Lyne
APPLICANT: CREELMAN, Robert A
APPLICANT: PINEDA, Omaira
APPLICANT: YU, Guo-Liang
APPLICANT: BROUN, Pierre E
TITLE OF INVENTION: Yield-Related Polynucleotides and Polypeptides in Plants
FILE REFERENCE: MB10036-2 US
CURRENT APPLICATION NUMBER: US/10/225,066A
CURRENT FILING DATE: 2002-08-09
PRIOR APPLICATION NUMBER: 09/837,444
PRIOR FILING DATE: 2001-04-18
PRIOR APPLICATION NUMBER: 60/310,847
PRIOR FILING DATE: 2001-08-09
PRIOR APPLICATION NUMBER: 60/336,049
PRIOR FILING DATE: 2001-12-05
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PRIOR APPLICATION NUMBER: 10/171,468
PRIOR FILING DATE: 2002-06-14
NUMBER OF SEQ ID NOS: 1122
SOFTWARE: PatentIn version 3.1
SEQ ID NO 128
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TYPE: PRT
ORGANISM: Arabidopsis thaliana
US-10-225-066A-128

Query Match 47.8%; Score 651; DB 18; Length 225;
Best Local Similarity 55.5%; Pred. No. 8.5e-52;
Matches 137; Conservative 31; Mismatches 49; Indels 30; Gaps 10;

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QY 1 MPTSDSGEPRIAMKPNP-----VTVPISDQEQQLPCPCDSSNTKFCYNNYNNFSQPRHF 56
DB 1 MP-SEFSSRRVPRKIPHGQGSVAIP-TDQEQQLSCPCESINTKFCYNNYNNFSQPRHF 58
QY 57 CKACRRYTHGTLRDVPGGTRKSAKRSRTCSNSSSVSGVNSNGVPLQTPVLF 116
DB 59 CKSCRRTYTHGTLRDIPVGVSRKSKRSRTYSSAATTSVVG-----SRNPPLQATPVLF 114
QY 117 POSSISNGVTHRTVESDQKGSALSLCGSFTSTLNNHNAATAATHGSGSVIGIGGIGLG 176
DB 115 POSSSNGGIT-----TAKGSASSFYGGF-SLLINYNAVSRNPGGFGFNGPDAGLGLG 167
QY 177 SG--FDDVSFGLGRAMPFSTVGT--ATTNVGSGHGAHPMPATWQFEGLESNAGGAF 232
DB 168 HGSYEDVRVYQGLITWPFSSGATDAATTS-----HIAQIPATWQFEGQESKV--GF 218
QY 233 VSGEYFA 239
DB 219 VSGDYVA 225

```

RESULT 5

US-10-424-599-268677
Sequence 268677, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: KOVALLIC David K
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated with
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53223)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 268677
LENGTH: 156
TYPE: PRT
ORGANISM: Glycine max
FEATURE:
OTHER INFORMATION: Clone ID: PAT_MRT3847_84638C.1.pep
US-10-424-599-268677

Query Match 32.0%; Score 436.5; DB 15; Length 156;
Best Local Similarity 55.1%; Pred. No. 3.7e-32;
Matches 92; Conservative 22; Mismatches 38; Indels 15; Gaps 6;

```

QY 1 MPTSDSGEPRIAMKP--NGVTVPISDQEQQLPCPCDSSNTKFCYNNYNNFSQPRHFCK 58
DB 1 MPSSNSGESRR-ASKPSSGGAADPPPEQENPPCPKCDSTVTKFCYNNYNNFSQPRHFCK 59
QY 59 ACRRYTHGTLRDVPGGTRKSAKRSRT--CSNSSSVSGVNSNGVPLQTPVLF 116
DB 60 SCRRTYTHGTLRDIPVGGGRKAKRSRTTHVAATSSSSGTCMTSAQEHART--LLA 117
QY 117 POSSISNGVTHRTVESDQKGSALSLCGSFTSTLNNHNAATAATHGSG 163
DB 118 PVASTHYGVLDGVDVQKTSNGG--NVCGSFTSLNN-----THSG 156

```

RESULT 6

US-10-225-066A-404
Sequence 404, Application US/10225066A
Publication No. US20030226173A1
GENERAL INFORMATION:
APPLICANT: Mendel Biotechnology, Inc.
APPLICANT: RATCLIFFE, Oliver
APPLICANT: RIECHMANN, Jose Luis
APPLICANT: ADAM, Luc J
APPLICANT: DUBBEL, Arnold T
APPLICANT: HEARD, Jacqueline E
APPLICANT: PILGRIM, Maretha L

```
APPLICANT: JIANG, Cai-Zhong
APPLICANT: REUBER, T. Lynne
APPLICANT: CREELMAN, Robert A
APPLICANT: PINEDA, Omaisra
APPLICANT: YU, Guo-Liang
APPLICANT: BROUN, Pierre E
TITLE OF INVENTION: Yield-Related Polynucleotides and Polypeptides in Plants
FILE REFERENCE: MB10036-2 US
CURRENT APPLICATION NUMBER: US/10/225,066A
CURRENT FILING DATE: 2002-08-09
PRIOR APPLICATION NUMBER: 09/837,444
PRIOR FILING DATE: 2001-04-18
PRIOR APPLICATION NUMBER: 60/310,847
PRIOR FILING DATE: 2001-08-09
PRIOR APPLICATION NUMBER: 60/336,049
PRIOR FILING DATE: 2001-12-05
PRIOR APPLICATION NUMBER: 60/338,692
PRIOR FILING DATE: 2001-12-11
PRIOR APPLICATION NUMBER: 10/171,468
PRIOR FILING DATE: 2002-06-14
NUMBER OF SEQ ID NOS: 1122
SOFTWARE: PatentIn version 3.1
SEQ ID NO 404
LENGTH: 209
TYPE: PR1
ORGANISM: Arabidopsis thaliana
US-10-225-066A-404
```

```
Query Match 29.5%; Score 402; DB 15; Length 209;
Best Local Similarity 39.0%; Pred. No. 8.3e-29;
Matches 101; Conservative 35; Mismatches 67; Indels 56; Gaps 13;
```

```
QY 1 MPTSDSGEPRIAMKNGVTVPISDOOEOLPCRCDSNTKFCYNNYNFSQPRHFKAC 60
D 1 MP-SEPNOTRPTTRQPSAIAAPPNLAELPCPCRCNSTTTKFCYNNYNLAQPRYYCKSC 59
QY 61 RRYWTHGCTLRDVPVGGGTRK-SAKRSRTCSN--SSSSSVGVNSNGVPLQTTPLVLP 117
D 60 RRYWTHGCTLRDVPVGGGTRSSSKRRHSFSTATSSSSSVITTTQBPATTEA---S 116
QY 118 QSSISNGVTHVTESDCKGSLSLCGSFTSTLLNHNAAATATGSGSVIGG--FGIGL 175
D 117 QTKVTNLIS-----GHGSFASLLGL-----GSGN---GGLDYGFY 149
QY 176 GSGFDVVSFG-IGRAMPFSTVGTATTNNVSGNGHHAVPMATWQFEGLESNAGGFFVS 234
D 150 GYGLEMSISGYLD-----SSVGEIPV--VDGCGD-----TWQIGETIEKSG----- 190
QY 235 GEYFAMPDLSITTPGNSLK 253
D 191 GDSLIMPGLGISMQTNDVK 209
```

```
RESULT 7
US-10-374-780A-2762
Sequence 2762, Application US/10374780A
Publication No. US2004001927A1
GENERAL INFORMATION:
```

```
APPLICANT: Sherman, Bradley K
APPLICANT: Riechmann, Jose Luis
APPLICANT: Jiang, Cai-Zhong
APPLICANT: Heard, Jacqueline E
APPLICANT: Haake, Volker
APPLICANT: Creelman, Robert A
APPLICANT: Ratcliffe, Oliver
APPLICANT: Adam, Luc J
APPLICANT: Reuber, T. Lynne
APPLICANT: Keddie, James
APPLICANT: Broun, Pierre E
APPLICANT: Pilgrim, Marsha L
APPLICANT: Dubell IT, Arnold T
APPLICANT: Pineda, Omaisra
APPLICANT: Yu, Guo-Liang
```

```
TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES IN PLANTS
FILE REFERENCE: MB1-0047 CIP
CURRENT APPLICATION NUMBER: US/10/374,780A
CURRENT FILING DATE: 2003-02-25
PRIOR APPLICATION NUMBER: 09/837,944
PRIOR FILING DATE: 2001-04-18
PRIOR APPLICATION NUMBER: 60/310,847
PRIOR FILING DATE: 2001-08-09
PRIOR APPLICATION NUMBER: 09/934,455
PRIOR FILING DATE: 2001-08-22
PRIOR APPLICATION NUMBER: 60/336,049
PRIOR FILING DATE: 2001-11-19
PRIOR APPLICATION NUMBER: 60/338,692
PRIOR FILING DATE: 2001-12-11
PRIOR APPLICATION NUMBER: 10/171,468
PRIOR FILING DATE: 2002-06-14
PRIOR APPLICATION NUMBER: 10/225,066
PRIOR FILING DATE: 2002-08-09
PRIOR APPLICATION NUMBER: 10/225,067
PRIOR FILING DATE: 2002-08-09
PRIOR APPLICATION NUMBER: 10/225,068
PRIOR FILING DATE: 2002-08-09
NUMBER OF SEQ ID NOS: 2906
SOFTWARE: PatentIn version 3.2
SEQ ID NO 2762
LENGTH: 209
TYPE: PR1
ORGANISM: Arabidopsis thaliana
FEATURE:
OTHER INFORMATION: G1898
US-10-374-780A-2762
```

```
Query Match 29.5%; Score 402; DB 15; Length 209;
Best Local Similarity 39.0%; Pred. No. 8.3e-29;
Matches 101; Conservative 35; Mismatches 67; Indels 56; Gaps 13;
```

```
QY 1 MPTSDSGEPRIAMKNGVTVPISDOOEOLPCRCDSNTKFCYNNYNFSQPRHFKAC 60
D 1 MP-SEPNOTRPTTRQPSAIAAPPNLAELPCPCRCNSTTTKFCYNNYNLAQPRYYCKSC 59
QY 61 RRYWTHGCTLRDVPVGGGTRK-SAKRSRTCSN--SSSSSVGVNSNGVPLQTTPLVLP 117
D 60 RRYWTHGCTLRDVPVGGGTRSSSKRRHSFSTATSSSSSVITTTQBPATTEA---S 116
QY 118 QSSISNGVTHVTESDCKGSLSLCGSFTSTLLNHNAAATATGSGSVIGG--FGIGL 175
D 117 QTKVTNLIS-----GHGSFASLLGL-----GSGN---GGLDYGFY 149
QY 176 GSGFDVVSFG-IGRAMPFSTVGTATTNNVSGNGHHAVPMATWQFEGLESNAGGFFVS 234
D 150 GYGLEMSISGYLD-----SSVGEIPV--VDGCGD-----TWQIGETIEKSG----- 190
QY 235 GEYFAMPDLSITTPGNSLK 253
D 191 GDSLIMPGLGISMQTNDVK 209
```

```
RESULT 8
US-10-225-066A-404
Sequence 404, Application US/10225066A
Publication No. US2005016049A9
GENERAL INFORMATION:
```

```
APPLICANT: Mendel Biotechnology, Inc.
APPLICANT: Ratcliffe, Oliver
APPLICANT: Riechmann, Jose Luis
APPLICANT: Adam, Luc J
APPLICANT: Dubell, Arnold T
APPLICANT: Heard, Jacqueline E
APPLICANT: Pilgrim, Marsha L
APPLICANT: Jiang, Cai-Zhong
APPLICANT: Reuber, T. Lynne
APPLICANT: Creelman, Robert A
APPLICANT: Pineda, Omaisra
```

APPLICANT: YU, Guo-Liang
APPLICANT: BROUN, Pierre E
TITLE OF INVENTION: Yield-Related Polynucleotides and Polypeptides in Plants
FILE REFERENCE: MB10036-2 US
CURRENT APPLICATION NUMBER: US/10/225,066A
PRIOR FILING DATE: 2002-08-09
PRIOR APPLICATION NUMBER: 09/837,444
PRIOR FILING DATE: 2001-04-18
PRIOR APPLICATION NUMBER: 60/310,847
PRIOR FILING DATE: 2001-08-09
PRIOR APPLICATION NUMBER: 60/336,049
PRIOR FILING DATE: 2001-12-05
PRIOR APPLICATION NUMBER: 60/338,692
PRIOR FILING DATE: 2001-12-11
PRIOR APPLICATION NUMBER: 10/171,468
PRIOR FILING DATE: 2002-06-14
NUMBER OF SEQ ID NOS: 1122
SOFTWARE: PatentIn version 3.1
SEQ ID NO 404
LENGTH: 209
TYPE: PRT
ORGANISM: Arabidopsis thaliana
US-10-225-066A-404

Query Match 29.5%; Score 402; DB 18; Length 209;
Best Local Similarity 39.0%; Pred. No. 8.3e-29;
Matches 101; Conservative 35; Mismatches 67; Indels 56; Gaps 13;

QY 1 MPTSDSGPRRIAMKPGVTVPISDQQLPCPRCDSSNTKFCYNNYNNFSGPRHCKAC 60
DB 1 MP-SEPNTRRPVRVQSTAAVPPVLAEPPLPCPRCNSITTKFCYNNYNNLQAPRYCKSC 59
QY 61 RRYTHGGTLADVPVGGGTRK-SAKRSRTCSN--SSSSSVGVSNSGVPLOTTPVLP 117
DB 60 RRYWTGGTLADVPVGGGTRKSSRRHRSFSTTATSSSSSVITTTQEPATTEA---S 116
QY 118 QSSISNGVTHVTESDGSALSLCGSFTSTLLNNAATATHGSGVIGIG--FGIGL 175
DB 117 QTKYTNLIS-----GHGSFASLIGL-----GSGN---GGLDYGFXY 149
QY 176 GSGFDVVSFG-LGRAMPFSTVGTATTNVSNGHAAVMPAPVQFGLSNAAGGFVS 234
DB 150 GYGLEMSIGYIGD-----SSVGEIPV--VDGCGD-----TWQIGEIFGKSG----- 190
QY 235 GEYFAMPDLSTTPGNSLK 253
DB 191 GDSLWPGLEISMOTNDVK 209

RESULT 9

US-10-225-066A-406
Sequence 406, Application US/10225066A
Publication No. US20030226173A1
GENERAL INFORMATION:
APPLICANT: Mendel Biotechnology, Inc.
APPLICANT: RATCLIFFE, Oliver
APPLICANT: RIECHMANN, Jose Luis
APPLICANT: ADAM, Luc J
APPLICANT: DUBELL, Arnold T
APPLICANT: HEARD, Jacqueline E
APPLICANT: PILGRIM, Marsha L
APPLICANT: JIANG, Cai-Zhong
APPLICANT: REUBER, T. Lynne
APPLICANT: CREELMAN, Robert A
APPLICANT: PINEDA, Omalra
APPLICANT: YU, Guo-Liang
APPLICANT: BROUN, Pierre E
TITLE OF INVENTION: Yield-Related Polynucleotides and Polypeptides in Plants
FILE REFERENCE: MB10036-2 US
CURRENT APPLICATION NUMBER: US/10/225,066A
PRIOR FILING DATE: 2002-08-09
PRIOR APPLICATION NUMBER: 09/837,444
PRIOR FILING DATE: 2001-04-18

PRIOR APPLICATION NUMBER: 60/310,847
PRIOR FILING DATE: 2001-08-09
PRIOR APPLICATION NUMBER: 60/336,049
PRIOR FILING DATE: 2001-12-05
PRIOR APPLICATION NUMBER: 60/338,692
PRIOR FILING DATE: 2001-12-11
PRIOR APPLICATION NUMBER: 10/171,468
PRIOR FILING DATE: 2002-06-14
NUMBER OF SEQ ID NOS: 1122
SOFTWARE: PatentIn version 3.1
SEQ ID NO 406
LENGTH: 204
TYPE: PRT
ORGANISM: Arabidopsis thaliana
US-10-225-066A-406

Query Match 27.7%; Score 377.5; DB 15; Length 204;
Best Local Similarity 48.8%; Pred. No. 1.5e-26;
Matches 83; Conservative 21; Mismatches 43; Indels 23; Gaps 5;

QY 26 QOEQLPCPRCDSSNTKFCYNNYNNFSGPRHCKACRRYTHGGTIRDPVGGGTRKSAKR 85
DB 25 EOELKCPKCDSPMTKFCYNNYNNLQAPRYCKSCRRRYTHGGALRNVPVGGGSKNATK 84
QY 86 SRTCSNSSSSSVGVSNSGVPLOTTPVLPPOSSISNGVTHT-----VTESDGKSA 138
DB 85 RSTSSSSASAPSN--SQNKTKAPDPDPKRSQKEDLPTKMLYGFPGDDVYK-- 140
QY 139 LSLGFTSTLLNNAATATHGSGVIGIGFGLT-GSGFDVVSFGL 187
DB 141 MEIGSFSLIANN-----MQLGLGGGIMLDGSGMDHGMQLG 179

RESULT 10

US-10-374-780A-362
Sequence 362, Application US/10374780A
Publication No. US20040019927A1
GENERAL INFORMATION:
APPLICANT: Sherman, Bradley K
APPLICANT: RIECHMANN, Jose Luis
APPLICANT: JIANG, Cai-Zhong
APPLICANT: HEARD, Jacqueline E
APPLICANT: HAAKE, Volker
APPLICANT: CREELMAN, Robert A
APPLICANT: RATCLIFFE, Oliver
APPLICANT: ADAM, Luc J
APPLICANT: REUBER, T. Lynne
APPLICANT: KEDDIE, James
APPLICANT: BROUN, Pierre E
APPLICANT: PILGRIM, Marsha L
APPLICANT: DUBELL III, Arnold T
APPLICANT: PINEDA, Omalra
APPLICANT: YU, Guo-Liang
TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES IN PLANTS
FILE REFERENCE: MB1-0047 CIP
CURRENT APPLICATION NUMBER: US/10/374,780A
CURRENT FILING DATE: 2003-02-25
PRIOR APPLICATION NUMBER: 09/837,944
PRIOR FILING DATE: 2001-04-18
PRIOR APPLICATION NUMBER: 60/310,847
PRIOR FILING DATE: 2001-08-09
PRIOR APPLICATION NUMBER: 09/934,455
PRIOR FILING DATE: 2001-08-22
PRIOR APPLICATION NUMBER: 60/336,049
PRIOR FILING DATE: 2001-11-19
PRIOR APPLICATION NUMBER: 60/338,692
PRIOR FILING DATE: 2001-12-11
PRIOR APPLICATION NUMBER: 10/171,468
PRIOR FILING DATE: 2002-06-14
PRIOR APPLICATION NUMBER: 10/225,066
PRIOR FILING DATE: 2002-08-09
PRIOR APPLICATION NUMBER: 09/837,444
PRIOR FILING DATE: 2002-08-09

```

; PRIOR APPLICATION NUMBER: 10/225,068
; PRIOR FILING DATE: 2002-08-09
; NUMBER OF SEQ ID NOS: 2906
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 362
; LENGTH: 204
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; OTHER INFORMATION: G1902 (conserved domain in AA coordinates:31-59)
US-10-374-760A-362

```

```

Query Match      27.7%; Score 377.5; DB 15; Length 204;
Best Local Similarity 48.8%; Pred. No. 1.5e-26;
Matches 83; Conservative 21; Mismatches 43; Indels 23; Gaps 5;

```

```

Qy 26 QOQLPCPRCDSSNTKFCYNNYNNFSGPRHFCACRRYTWHTGTLRDVPGGTRKSAKR 85
    :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 25 EOQLKPCRCDSNPKFCYNNYNNLSQPRHFCSCRRYTWKGALRVNVPVGGSRKNATK 84
    :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 86 SRTCSNSSSSVSGVNSNGVPLQTPVLFPOSSISNGVTHT-----VTESDGKSA 138
    :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 85 RSTSSSSASAPSN--SQNKKTKNPDPPDRNSQKRPDLPTRMLYGFPFGDDVVG-- 140
    :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 139 LSLGSGFTSTLLNMAATATHGSGSVIGIGFGIGL-GSGFDDVSFGLG 187
    :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 141 MEIGGSFSSLANN-----MQLGIGGGIMLDGSGMDHPGMGLG 179
    :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

```

```

RESULT 11
US-10-225-066A-406
; Sequence 406, Application US/10225066A
; Publication No. US20050160493A9
; GENERAL INFORMATION:
; APPLICANT: Mendel Biotechnology, Inc.
; APPLICANT: RATCHFEE, Oliver
; APPLICANT: RIECHMANN, Jose Luis
; APPLICANT: ADAM, Luc J
; APPLICANT: DUBBEL, Arnold T
; APPLICANT: HEARD, Jacqueline E
; APPLICANT: PILGRIM, Marsha L
; APPLICANT: JIANG, Cai-Zhong
; APPLICANT: REUBER, T. Lynne
; APPLICANT: CREELMAN, Robert A
; APPLICANT: PINEDA, Omalra
; APPLICANT: YU, Guo-Liang
; APPLICANT: BROUN, Pierre E
; TITLE OF INVENTION: Yield-Related Polynucleotides and Polypeptides in Plants
; FILE REFERENCE: MEI0036-2 US
; CURRENT APPLICATION NUMBER: US/10/225,066A
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: 09/837,444
; PRIOR FILING DATE: 2001-04-18
; PRIOR APPLICATION NUMBER: 60/310,847
; PRIOR FILING DATE: 2001-08-09
; PRIOR APPLICATION NUMBER: 60/336,049
; PRIOR FILING DATE: 2001-12-05
; PRIOR APPLICATION NUMBER: 60/338,692
; PRIOR FILING DATE: 2001-12-11
; PRIOR APPLICATION NUMBER: 10/171,468
; PRIOR FILING DATE: 2002-06-14
; NUMBER OF SEQ ID NOS: 1122
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 406
; LENGTH: 204
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-225-066A-406

```

```

Query Match      27.7%; Score 377.5; DB 18; Length 204;
Best Local Similarity 48.8%; Pred. No. 1.5e-26;
Matches 83; Conservative 21; Mismatches 43; Indels 23; Gaps 5;

```

```

Qy 26 QOQLPCPRCDSSNTKFCYNNYNNFSGPRHFCACRRYTWHTGTLRDVPGGTRKSAKR 85
    :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 25 EOQLKPCRCDSNPKFCYNNYNNLSQPRHFCSCRRYTWKGALRVNVPVGGSRKNATK 84
    :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 86 SRTCSNSSSSVSGVNSNGVPLQTPVLFPOSSISNGVTHT-----VTESDGKSA 138
    :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 85 RSTSSSSASAPSN--SQNKKTKNPDPPDRNSQKRPDLPTRMLYGFPFGDDVVG-- 140
    :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 139 LSLGSGFTSTLLNMAATATHGSGSVIGIGFGIGL-GSGFDDVSFGLG 187
    :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 141 MEIGGSFSSLANN-----MQLGIGGGIMLDGSGMDHPGMGLG 179
    :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

```

```

RESULT 12
US-10-425-114-40748
; Sequence 40748, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jindong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 40748
; LENGTH: 206
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB25-078-G1_FLI.pep
US-10-425-114-40748

```

```

Query Match      27.7%; Score 377.5; DB 15; Length 206;
Best Local Similarity 48.8%; Pred. No. 1.5e-26;
Matches 83; Conservative 21; Mismatches 43; Indels 23; Gaps 5;

```

```

Qy 26 QOQLPCPRCDSSNTKFCYNNYNNFSGPRHFCACRRYTWHTGTLRDVPGGTRKSAKR 85
    :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 27 EOQLKPCRCDSNPKFCYNNYNNLSQPRHFCSCRRYTWKGALRVNVPVGGSRKNATK 86
    :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 86 SRTCSNSSSSVSGVNSNGVPLQTPVLFPOSSISNGVTHT-----VTESDGKSA 138
    :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 87 RSTSSSSASAPSN--SQNKKTKNPDPPDRNSQKRPDLPTRMLYGFPFGDDVVG-- 142
    :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 139 LSLGSGFTSTLLNMAATATHGSGSVIGIGFGIGL-GSGFDDVSFGLG 187
    :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 143 MEIGGSFSSLANN-----MQLGIGGGIMLDGSGMDHPGMGLG 181
    :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

```

```

RESULT 13
US-10-424-599-187121
; Sequence 187121, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 187121
; LENGTH: 211
; TYPE: PRT
US-10-424-599-187121

```

ORGANISM: Glycine max
FEATURE:
OTHER INFORMATION: Clone ID: PAT_MRT3847_139983C.1.pap
US-10-424-599-187121

Query Match 27.6%; Score 376.5; DB 15; Length 211;
Best Local Similarity 39.8%; Pred. No. 1.9e-26;
Matches 96; Conservative 25; Mismatches 77; Indels 43; Gaps 8;

QY 18 GVTVPISDQEQQLPCPRCDSSNTKFCYNNYNFSPQPHFCCKACRRYTHGGTLRDVPGG 77
DB 9 GVKPQPEQEQQLKPCPCDSNNTKFCYNNYNLSQPHFCCKACRRYTHGGTLRNIPVGG 68
QY 78 GTRKSAKRSRT--CNSSSSSSVSVSNNGVPLQTPPLFPOSSISNGVTHVTYESDOK 135
DB 69 GSRKTTKSSSTLSKRSAPSSSAVSDPDPRTCTNPVDOQVNLNG----- 117
QY 136 GSALSLCGSFTSTLLNHNAAATATG--SGSVIGIGGFGIGLGSGFDDVSFGLGRAMWP 192
DB 118 -----GGSFSSLLASGHHFTLLGLNPSGSLKMGGEFVSS--DPGLNLSGLNP 168
QY 193 FSTVGTATTNNVSGNGHHAVMPATWQFEGLESNAGGFVSGEYFAMPDLSTTPGNSL 252
DB 169 -----DLQVQSNENSES-----FLGIQ-NGDSSCWNGTH-GMSDLATYTPGPSF 210
QY 253 K 253
DB 211 Q 211

RESULT 14
US-10-425-114-43084
Sequence 43084, Application US/10425114
Publication No. US20040034888A1

GENERAL INFORMATION:
APPLICANT: Liu, Jindong
APPLICANT: Zhou, Yihua
APPLICANT: Kovalic, David K.
APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(5313)B
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 43084
LENGTH: 211
TYPE: PRT
ORGANISM: Glycine max
FEATURE:
OTHER INFORMATION: Clone ID: 700685541_FLI.pap
US-10-425-114-43084

Query Match 27.6%; Score 376.5; DB 15; Length 211;
Best Local Similarity 39.8%; Pred. No. 1.9e-26;
Matches 96; Conservative 25; Mismatches 77; Indels 43; Gaps 8;

QY 18 GVTVPISDQEQQLPCPRCDSSNTKFCYNNYNFSPQPHFCCKACRRYTHGGTLRDVPGG 77
DB 9 GVKPQPEQEQQLKPCPCDSNNTKFCYNNYNLSQPHFCCKACRRYTHGGTLRNIPVGG 68
QY 78 GTRKSAKRSRT--CNSSSSSSVSVSNNGVPLQTPPLFPOSSISNGVTHVTYESDOK 135
DB 69 GSRKTTKSSSTLSKRSAPSSSAVSDPDPRTCTNPVDOQVNLNG----- 117
QY 136 GSALSLCGSFTSTLLNHNAAATATG--SGSVIGIGGFGIGLGSGFDDVSFGLGRAMWP 192
DB 118 -----GGSFSSLLASGHHFTLLGLNPSGSLKMGGEFVSS--DPGLNLSGLNP 168
QY 193 FSTVGTATTNNVSGNGHHAVMPATWQFEGLESNAGGFVSGEYFAMPDLSTTPGNSL 252

DB 169 -----DLQVQSNENSES-----FLGIQ-NGDSSCWNGTH-GMSDLATYTPGPSF 210
QY 253 K 253
DB 211 Q 211

RESULT 15
US-10-424-599-239234
Sequence 239234, Application US/10424599
Publication No. US20040031072A1

GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J
APPLICANT: Kovalic, David K
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated with
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53223)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 239234
LENGTH: 211
TYPE: PRT
ORGANISM: Glycine max
FEATURE:
OTHER INFORMATION: Clone ID: PAT_MRT3847_58053C.1.pap
US-10-424-599-239234

Query Match 26.1%; Score 356; DB 15; Length 211;
Best Local Similarity 36.4%; Pred. No. 1.5e-24;
Matches 92; Conservative 28; Mismatches 65; Indels 68; Gaps 10;

QY 14 MKPENGTVIPISDQEQQLPCPRCDSSNTKFCYNNYNFSPQPHFCCKACRRYTHGGTLRDV 73
DB 10 MKPH-----PPEQEQQLKPCPCDSNNTKFCYNNYNLSQPHFCCKACRRYTHGGTLRNIPVGG 63
QY 74 PVGGTRKSAKRSRTCSNNSSSSVSVSNNGVPLQTPPLFPOSSISNGVTHVTYESD 133
DB 64 PVGGSRKTRKSSSSNNNTYRA-----SPSPVSSAPAPEDPT-RIGPTPV----- 111
QY 134 GKSALSLCGSFTSTLLNHNAAATATGSGSVIGIGGFGIGLGSGFDDVSFGLGRAMWP 193
DB 112 --G-----GGSFSSLL-----ASSG-----LGLNLSGLNPS-----G 139
QY 194 FSTVGTATTNNVSGNGHHAVMPATWQFEGLESNAGGFVSGEYF----- 238
DB 140 SNLKTQWEEFGEVNSGFPVADPDGSRNPGLEMQSNG--NAESFLSLQNGDSCGCGN 196
QY 239 AMPDLSTTPGNS 251
DB 197 GMSDLATYTPGPS 209

Search completed: November 3, 2005, 16:17:25
Job time : 168 secs

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